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Contact: Turkewitz AP
Molecular Genetics and Cell Biology
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Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
[ (basea 1 to 11)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Erankel, J. and Klobutcher, L.

EST from Terrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. Selb Street, Chicago

921 E. Selb Street, Chicago
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Bukaryota, Alveolata, Cillophora, Oligohymenophorea;

Hymenostomatida; Tetrahymenina, Tetrahymena.

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S Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

Frankel,J. and Klobuccher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz A.P.

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University of Chicago

20 E. S&th Street, Chicago, IL 60637, USA

Tel: 773 702 3172

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.
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Frankel, J. and Klobutcher, L.
EST from Terrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago, IL 60637, USA
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/organism="Homo sapie /mol_type="unassignec /db_xref="taxon:9606	Query Match 66.4%; Score 16 Best Local Similarity 84.0%; Pred. No Matches 21; Conservative 0; Misma	2y 3 GGCCTACGTGTACAGGAGTCCAG 2'			ACCESSION AX890110 VERSION AX690110.1 GI:29412968 KEYWORDS	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa;		AUTHORS Shannon,M., Gu,Y. and Nguyen,( TITLE Four human zinc-finger-contain	JOURNAL Patent: EP 1281758-A 2842 05-1	FEATURES ACOUNTED, 105, 105, 105, 105, 105, 105, 105, 105	/organism="Homo sapi; /mol_type="unassigne"	/db_xref="taxon:9606	N W	Macciles ZI; Collservacive U; Mis	4 GCCCTACGTGTACAGGGAGTCCAGG	Db 1 GCCCTACGTGCAGCGAGTGCTGG 2	RESULT 3	AX690107	DEFINITION Sequence 2839 from Patent EP1 ACCESSION AX690107 VERSION AX690107.1 GI:29412965	Homo sapiens (human)	OKGANISM HOMO Sapiens Eukaryota, Matazoa; Chordata; Mammalia: Butheria; Primates;	Gu, Y. an zinc-fing	mdz12 JOURNAL Patent: BP 1281758-A 2839 05-	FEATURES Location/Qualifiers source 125	/organism="Homo sapi /mol_type="unassigne /db_xref="teaxon:9606"			9 GCCCTACGIGIACAGGAGICC 25
ACCESSION:AX624330 ACCESSION:AX624837 ACCESSION:AX626047 ACCESSION:AX625403	ACCESSION: AX625794 ACCESSION: AX626034 ACCESSION: AX626752	ACCESSION: AX6.26783 ACCESSION: AX6.2688 ACCESSION: AX627660 ACCESSION: AX627965	ACCESSION: AX628121 ACCESSION: AX628521 ACCESSION: AX628699	ACCESSION: AX629205 ACCESSION: AX629571 ACCESSION: AX629648	ACCESSION:AX629882 ACCESSION:AX630279 ACCESSION:AX631061	ACCESSION: AX631445 ACCESSION: AX631751 ACCESSION: AX632258	ACCESSION:AX632468 ACCESSION:BD124405	ACCESSION: BD12441 ACCESSION: A47665	ACCESSION: AROLA 90 ACCESSION: AROLA 983 ACCESSION: AROLA 90	ACCESSION: EASIS ACCESSION: E29545 ACCESSION: E38651	ACCESSION: 123754	ACCESSION: 135021 ACCESSION: AR224412	ACCESSION: AX073609 ACCESSION: AX073609	ACCESSION: AXA 54105	ACCESSION: AX454110 ACCESSION: BD023278	ACCESSION: AX690109 ACCESSION: AX690110	ACCESSION: AX690107 ACCESSION: AX690108	ACCESSION: AX690111 ACCESSION: AX690112	ACCESSION: AX096928	NTS		25 bp DNA linear PAT 31-MAR-2003 3P1281758.		Craniata, Vertebrata, Euteleostomi,	ırrhını	ng proteins : mdz3, mdz4, mdz7 and	-FBB-2003;	
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Aeomica, Inc. (US)
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   AX690106.1 GI:29412964
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
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Unclassified.

I (bases 1 to 21)

S Hilton, D. James.

Mouse interleukin-11 receptor

AL Patent: US 6274708-A 19 14-AUG-2001;

Location/Qualifiers

Location/Qualifiers
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Aeomica, Inc. (US)
Location/Qualifiers
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17 bp DNA Sequence 1337 from Patent EP1281758.
Score 14.4; DB;
Pred. No. 11;
0; Mismatches
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Sequence 1336 from Patent EP1281758.
AX688604
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I Similarity 84.2%; Pred. No. 19;
16; Conservative 0; Mismatches

    .17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 19 from patent US 6274708.
AR165205.
AR165205.1 GI:16238680
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Query Match
Best Local Similarity 93.8%;
Matches 15; Conservative C
                                                           3 GGCCCTACGTGTACAG 18
                                                                                   2 GGCCCTACGTGTGCAG 17
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Matches 16; Conserva
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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82.6%; Pred. No. 7.5;
iive 0; Mismatches 4;
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Best, Local Similarity 90.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 2;
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 mdz12
Patent: EP 1281758-A 2836 05-FEB-2003;
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Aeomica, Inc. (US)
Location/Qualifiers
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Reomica, Inc. (US)
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Sequence 2844 from Patent EP1281758.
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EP1281758.
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/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
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    .25
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/db_xref="taxon:9606"

                               Inc. (US)
Location/Qualifiers
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Sequence 1335 from Patent
AX688603
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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AX688602
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Patent: EP 1281758-A 1339 05-FEB-2003;
Acomica, Inc. (US)
Location/Qualifiers
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Aeomica, Inc. (US)
Location/Qualifiers
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Aeomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches
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Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Acomica, Inc. (US)
                                                                                                                                                                                 Sequence 1339 from Patent EP1281758. AX688607 GI:29411309
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AX688606
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Best Local Similarity 88.2%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches

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Shannon, M., Gu, Y. and Nguyen, C.T.
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Location/Qualifiers
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PAT 27-AUG-2002

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AB069243 11-MAY-2003 Synthetic construct DNA, reverse primer for human STS sts-L07033 at
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JP 2001321190-A/710
20-NOV-2001
12-MAR-2001
BIICHI SOEDA
C12N15/09,C12N15/09,C12N1/00,C12Q1/68,G01N33/53,G01N33/566,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soeda,E.
A method of arraying genome clone
Patent: JP 200121190-A 710 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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Docation/Qualifiers
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                                                      Padigaru, M., Mezes, P., Mishra, V., Burgess, C., Casman, S., Grosse, W.M., Alsobrook, J.P., Lepley, D.M., Gerlach, V.L., Macdougall, J.R. and Smithson, G.
Proteins and nucleic acids encoding same Patent: WO 0210216-A 35 07-FEB-2002;
Curagen Corporation (US)
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83.3%; Pred. No. 27;
ive 0; Mismatches 3;
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/db_xref="taxon:32630"
/note="0ligonucleotide primers"

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        /organism="synthetic construct"
/mol type="genomic DNA"
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Matches 14; Conservative
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Matches 15; Conservative
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Unknown.
Unclassified.
Unclassified.
I (bases 1 to 18)
Barrett, G.Leelie.
Method for enhancing neurone survival and agents useful for same Method for enhancing neurone survival and agents useful for same Patent: US 6174869-A 6 16-JAN-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                            Tobses 1 to 18)
Barrett,G.Leslie.
Method for enhancing neurone survival and agents useful for same Patent: US 5837694-A 6 17-NOV-1998;
Location/Qualifiers
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Best Local Similarity 93.3%; Pred. No. 21;
Matches 14; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 93.3%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches
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Sequence 35 from Patent W00210216.
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AX449606.1 GI:21698215
                                                                                                                                                                      Sequence 6 from patent US 5837694.
AR058208
. GI:5983785
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/organism="unknown"
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Print DNA linear PAT 31-JAN-2002 slimer DNA and method for detecting mRNA encoding prostate gland-specific antigen by using the same.
                                                                                           PAT 31-MAR-2003
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
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Unidentified
unidentified
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E 1 (bases 1 to 19)
S Nakagawara.H.
Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same
L Patent: JP 2000069969-A 4 O7-MAR-2000;
HITACHI CHEMICAL CO LTD, KK NIHON IDENSHI KENKYUJO
OS Unidentified
PN JP 2000069969-A/4
PD 07-MAR-2000
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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/organism='Unidentified'
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11arity 87.5%; Pred. No. 33;
Conservative 0; Mismatches 2;
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                                                                                     Sequence 1341 from Patent EP1281758. AX688609

    1.17
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Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches
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C12N15/09,C12Q1/68,C12N15/00
Strandedness: Single;
Topology: Linear;
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20 CGTGTGTAGGGAGTCCGG
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                                                                                                                                                   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushina,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.
A BAC-based STS-content map spanning a 35-Mb region of human
                                                                                                                                                                                                                                                                                                                                                                Direct Submission

Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)

Location/Qualifiers
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| | wol_type="unassigned DNA"
| db_xref="taxon:33630"
| note="Hypothetical Probe Sequence"
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/mol_type="genomic DNA"
/b_xref="taxon:32630"
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Sequence 9238 from Patent WO0179548.
AX297476
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Genomics 74 (1), 55-70 (2001)
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AB069243.1 GI:15130047
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AX419938
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                                                                                                                                                                                                                                                                       Shannon,M., Gu,Y. and Nguyen,C.T. Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Method and reagent for inhibiting HBV viral replication Patent: EP 1288296-A 484 05-MAR-2003;
RIBOZYME PHARACEUTICALS, INC. (US)
Location/Qualifiers
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    /organism="synthetic construct"
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    /noTe="Nucleic acid clone fragments"

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Aeomica, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
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Sequence 484 from Patent EP1288296.
AX711184
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synthetic construct
artificial sequences.
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Homo sapiens
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                   CCTACGTGTACAGGGA
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Best Local Similarity
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13; Conserv
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Patent: Wo 0198537-A 275 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
Location/Qualifiers
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North, M., Nishina, P., Naggert, J. and Noben-Trauth, K. Gene family associated with neurosensory defects
Patent: US 6114502-A 30 05-SEP-2000;
Location/Qualifiers
Unknown.
Unclassified.
Unclassified.
1 (bases i Lo. 19)
North, M. Nishina, P., Noben-Trauth, K. and Naggert, J.
Obesity associated genes
Patent: US 5776/62-A 18 07-JUL-1998;
Location/Qualifiers
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Best Local Similarity 92.9%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 1; Indels
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    17
/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"

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Sequence 275 from Patent WO0198537.
AX419938
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    .19
    /organism="unknown"
    /mol_type="unassigned DNA"

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/wol_type="unassigned DNA"
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PAT 17-JUL-2003

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1 (bases 1 to 18)
Evans, G.A. and Smith, M.W.
Brans, G.A. and Smith, M.W.
Method for generation of sequence sampled maps of complex genomes
Patent: US 5851760-A 129 22-DEC-1998;
Location/Qualifiers
                                                                                                                        Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unclassified.
1 (bases 1 to 18)
Meek,K.D.
Genetic test for equine severe combined immunodeficiency disease
Patent: US 5976803-A 6 02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 43.6%; Score 12.2; DB 1; Length 18; Best Local Similarity 82.4%; Pred. No. 41; Matches 14; Conservative 0; Mismatches 3; Indels
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Human prostate cancer candidate protein 1
Patent: WO 03050284-A 2304 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
Location/Qualifiers
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Sequence 129 from patent US 5851760.
AR066781
                                  AX783973 17 bp DNA
Sequence 2304 from Patent WO03050284.
AX783973.1 GI:32951822
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82.4%; Pred. No. 36;
tive 0; Mismatches
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    .17
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Sequence 6 from patent US 5976803.
AR083092 GI:10009882
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Matches 14; Conservative
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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43.6%; Score 12.2; DB 1; Length 17;
8est Local Similarity 82.4%; Pred. No. 36;
4atches 14; Conservative 0; Mismatches 3; Indels
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                      DB 1; Length
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Patent: WO 03050284-A 2159 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
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AX783828
AX783828.1 GI:32951677
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Acomica, Inc. (US)
Location/Qualifiers
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Best Local Similarity 82.4%; Pred. No. 36;
Matches 14; Conservative 0; Mismatches
                     Score 12.2; DE
Pred. No. 36;
0; Mismatches
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/organism="Homo sapiens"
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Sest Local Similarity 82.4%;
fatches 14; Conservative
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Paulussen, A.D. and Armstrong, M.
Genotyping cytochrome expression
Patent: W0 013332-A 2 06-JUL-2000;
JANSSEN PHARMGUTICA NV (BE) ; PAULUSSEN ALMEE DYMPHNE CATHER (BE)
; ARMSTRONG MARTIN (GB)
Location/Qualifiers
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Synthetic construct

synthetic construct

a tificial sequences.

E 1 (bases 1 to 16)

S Paulussen, A.D.C. and Armstrong, M.

Genotyping cytochrome expression

L JANSEN PHARMACTUTICA NV

OS Artificial Sequence

PN 07 2002533136-A2

PN 22-DEC-1999 UP 2000591220

PR 22-DEC-1999 GB 9828619.6

PR 23-DEC-1999 GP 2001033/53, G01N33/566, C12N15/00 CC

C12N15/09/C12Q1/02, C12Q1/68, G01N33/556, C12N15/00 CC

Description of Artificial Sequence: primer

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Location/Qualifiers
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42.1%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels
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/mol type="genomic DNA"
/db_xref="taxon:32630"
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42.1%; Score 11.8; I
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches
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Sequence 2 from Patent W00039332.
AX026612 AX026612.1 GI:10187786
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Genotyping cytochrome expression.
ED246816
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JP 2002533136-A/2.
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artificial sequences.
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AX026612
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shannon,M., Gu,Y. and Nguyen,C.T. Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
                                                                                                                                                                                                                                                                                                                                                                                                                                    Shannon,M., Gu,Y. and Nguyen,C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                Length 18;
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43.6%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3;
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Aeomica, Inc. (US)
Location/Qualifiers
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Acomica, Inc. (US)
Location/Qualifiers
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Sequence 1332 from Patent EP1281758.
AX688600
AX688600.1 GI:29411302

    1.17
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Sequence 1331 from Patent EP1281758.
AX688599 1G1:29411301

    17 'l7 'lorganism="Homo sapiens" 
/mol_type="unassigned DNA" 
/db_xref="taxon:9606"

                   1. .18
/organism="unknown"
/mol_type="unassigned DNA"
 Location/Qualifiers
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Homo sapiens
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Best Local Similarity 100.
Matches 12; Conservative
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6 GGCCCTACGTGT 17
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PAT 29-SEP-1999

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Tamb,A..
Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes Patent: US 5801236-A 23 01-SEP-1998;
Location/Qualifiers
1. 16
/organism="unknown"
/mol_type="unassigned DNA"
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1 (bases 1 to 16)

2 Kolnick,M.H., Cannon-Albright,L.A. and Kamb,A.

Methods for detecting predisposition to cancer at the MTS patent: US 5989815-A 23 23-NOV-1999;

Location/Qualifiers
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Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3;
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Unknown.
Unclassified.
E 1 (bases 1 to 16)
(S Stone, S., Jiang, P. and Kamb, A.
Mouse WYS! gene
Mouse WYS! gene
(AL Patent: US 5843756-A 23 01-DEC-1998;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 23 from patent US 5989815.
AR087871
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/mol_type="unassigned DNA"
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Sequence 23 from patent US 5843756.
AR062793 17:5990484
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1 (bases 1 to 16)
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AR087871
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Method and reagent for inhibiting HBV viral replication Fatent: EP 1288296-A 482 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
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/organism="synthetic construct"
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/note="Nucleic acid clone fragments"
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81.2%; Pred. No. 54;
iive 0; Mismatches 3;
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MTS1E1.beta. gene
Patent: US 5739027-A 23 14-APR-1998;
Location/Qualifiers
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Sequence 23 from patent US 5801236.
AR037513
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Sequence 482 from Patent EP1288296.
AX711182
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/organism="unknown"
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1 (bases 1 to 16)
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity 81.2%; Pred. No. 54;
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Patent: US 6218146-A 23 17-APR-2001;
Location/Qualifiers
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1 (bases 1 to 16)
Stone,S., Jang,P. and Kamb,A.
Mouse MTS2 gene
Patent: US 6210949-A 23 03-APR-2001;
Location/Qualifiers
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/organism="unknown"
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40.0%; Score 11.2; I
Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches
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Sequence 23 from patent US 6210949,
AR144933
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/mol_type="unassigned DNA"
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Sequence 23 from patent US 6218146.
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Location/Qualifiers
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1 (bases 1 to 16)
Kamb, A.
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M Unclassified.

B 1 (bases 1 to 16)

Ks Kamb, A.

Antibodies specific for MTS2 Polypeptide

AL Patent: US 6140473-A 23 31-OCT-2000;

Location/Qualifiers

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40.0%; Score 11.2; DB 1;
Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3;
                                                                  DNA
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WTS2 gene
Patent: US 5994095-A 23 30-NOV-1999;
Location/Qualifiers
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WTS2 gene
Patent: US 6180776-A 23 30-JAN-2001;
                                                             16 bp
Sequence 23 from patent US 5994095.
AR091341.
AR091341.1 GI:10018096
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Sequence 23 from patent US 6180776.
AR127766.1 GI:14114361
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  1 CGTGTCCAGGAAGCCC 16
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                         Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2951 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
                                                                                                                                                                                                                                Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2950 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Matches 13; Conservative 0; Mismatches 3;
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AX688611
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Sequence 2951 from Patent WO0173002.
AX265560
                                          17 bp DN
Sequence 2950 from Patent WO0173002.
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AX265559.1 GI:16514358
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AX265560
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AX688611
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PR 12-APR-1999 US 60/123990
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC PC PC
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(C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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unclassified.
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Breptlation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 7217 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Skolnick M.H., Cannon-Albright, L.A. and Kamb, A. Germline mutations in the MTS gene
Patent: US 5624819-A 23 29-APR-1997;
Location/Qualifiers
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Pred. No. 61;
0; Mismatches
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141167
141167.1 GI:2081757
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JP 2002541795-A/7217
10-DEC-2002
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A61K37/02, (C12N5/00,C12R1:91)

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Query Match
Best Local Similarity 81.2%;
Matches 13; Conservative (

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AX783974/c
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AX783972/c
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                               Shannon,M., Gu,Y. and Nguyen,C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: W0 03050284-A 2160 19-UUN-2003;
Amersham Biosciences (SV) Corp. (US)
Location/Qualifiers
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                                                                                         Patent: EP 1281758-A 1343 05-FEB-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 2160 from Patent WO03050284.
AX783829
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/db_xref="taxon:9606"

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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 03050284-A 2305 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
Location/Qualifiers
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Sequence 2303 from Patent WO03050284.
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Seguence 2305 from Patent WO03050284.
AX783974
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81.2%; Pred. No. 61;
ive 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
40.0%; Score 11.2; Ilarity 81.2%; Pred. No. 61; Conservative 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                        PAT 29-SEP-1999
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Unclassified.
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1 (bases 1 to 15)
Draper.K.G.
Method and reagent for inhibiting hepatitis C virus replication
Patent: US 6132966-A 121 17-OCT-2000;
Location/Qualifiers
                                                                                                                  1 (bases 1 to 15)
Draper, K.G.
Method and reagent for inhibiting hepatitis C virus replication
Patent: US 586253-A 121 09-FEB-1999;
Location/Qualifiers
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Draper.

Enzymatic RNA molecule targeted against Hepatitis C virus
Patent: US 5610054-A 121 11-MAR-1997;

Location/Qualifiers
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Sequence 121 from patent US 5610054.
IS7584.
IS7584.1 GI:2482648
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                       AR033355
Sequence 121 from patent US 5869253.
AR033355.
AR033355.1 GI:5948960
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Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches
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38.6%; Score 10.8; I
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches
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/organism="unknown"
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B Blatt.i., Mcwarggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
S Blatt.i., Mcwarggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
L. Patent: JP 2002512791-A 678 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PR JP 2002512791-A/678
PP 26-APR-1999 UP 200545991
PR 27-APR-1999 US 60/083217,18-SEP-1999 US 60/100842 PR
25-FEB-1999 US 09/25/608,23-MAR-1999 US 09/274553 PI
LAMRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
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C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
A61K37/66,
C12N15/00
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Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W. Gene expression profiles in normal and cancer cells Patent: US 6333152-A 637 25-DEC-2001;
Location/Qualifiers
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Seguence 637 from patent US 6333152.
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Pred. No. 58;
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JP 2002512791-A/678.
unidentified
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AR180569.1 GI:2022602
                                                                th 38.6%;
1 Similarity 85.7%;
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Matches 12; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Draper, K.G.
Method and reagent for inhibiting hepatitis C virus replication
Patent: US 5862253-A 297 09-FEB-1999;
Location/Qualifiers
Method for determining skin stress or skin ageing in vitro Patent: WO 02053773-A 102 11-JUL-2002; HENKEL KGAA (DE) Location/Qualifiers
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Sequence 6247 from Patent W002053774.
AX629206.
AX629206.1 GI:28457244
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Bukaryota; Asconayocta; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetae; Saccharomycetes;
Chases I to 10

S Ucloulesou, V. E., Vogelstein, B. and Kinzler, K. W.
Characterization of the yeast transcriptome
L Patent: JP 2001509017-A 256 10-JUL-2001;
FR JOHNS HOPKINS UNIVERITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
FR 22-JAN-1999 UP 1998332117
FR 23-JAN-1999 US 60/035917
FR 23-JAN-1999 US 60/035917
FR Z3-GAN-1999 US 60/035917
FR Z3-GAN-1999 US 60/035917
CLINIS/10,CLINIS/31,COTAK4/395,CLIOL/68,CLIOL/62 CC
Characterization of the yeast transcriptome
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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    15 / Organism='Hepatitis C

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/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"
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Characterization of the yeast transcriptome.
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JP 20101509017-4/256.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
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Hofmann,K., Conradt,M. and Petersohn,D.
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Sequence 102 from Patent W002053773.
AX470525
AX470525.1 GI:22205650
                                                                                                                                                                           Query Match 38.6%; Score 10.8; I
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches

    .15
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/mol_type="genomic RNA"
/db_xref="taxon:32644"

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                                         virus)'
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Homo sapiens
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BD207264
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AX635280
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                                                                     PAT 16-MAY-2001
                                                                                                                                                   Unclassified.

1 (Dases 1 to 15)
Draper,K.G.
Method and reagent for inhibiting hepatitis C virus replication
Patent: US 6132966-A 297 17-OCT-2000;
Location/Qualifiers
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Sullivan, S., Draper, K.G., McSwiggen, J. and Stinchcomb, D.T.
IL-5 targeted ribozymes
Patent: US 5616488-A 4 01-APR-1997;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 15)
Draper,K.G.
Enzymatic RNA molecule targeted against Hepatitis C virus
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Sequence 297 from patent US 6132966.
AR113353.
AR113353.1 GI:14093675
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 24 from patent US 5616488.
138986
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/organism="unknown"
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BD207264 17-JUL-2003 Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
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Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
to hepatitis cutled acid treatment of diseases or conditions related
to hepatitis C virus infection
Patent: JP 2002512791-A 854 08-MAY-2002;
RIBOZYME PHRAMAGEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A 854
PD 08-MAY-2002
PP 26-APR-1999 UP 2000545991
PR 27-APR-1999 US 60/083217,18-SEP-1999 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stinchcomb, D.T., Dudycz, D.W., Chowrira, B., Grimm, S., Direnzo, A., Karpelsky, A., Daper, K.G., Kislch, K., Matulic-Adamic, J. Moswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.W., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
Patent: US 5610054-A 297 11-MAR-1997;
Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
                                                                                  /organism="unknown"
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KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11, C07H21/04, A61K31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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Guo, B. and Sun, X.
Method for genotyping of single nucleotide polymorphism
Patent: US 6479242-A 38 12-NOV-2002;
Location/Qualifiers
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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONOCIECTIDE PREPARATION METHOD
PALENT: WO 9833904-A 884 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
LOCALION/QUALIFIEES
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/organism='Unknown'
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    .14
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JP 2001511000-A/884.
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l Similarity 84.6%;
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Brysch,W.

PHRANACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVARIACION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS

CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS

Bacent, W. 9520261-A 61 19-7AN-1995,

BICGNOSTIK GES FUER BICOMOLEKUL (DE)

Other publication AU 7345694 950206.
                                            DENNIS MACEJAK
C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
A61K37/06
C12N15/00
Enzymatic nucleic acid treatment of diseases or conditions C
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1 (bases 1 to 14)
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    /organism='Hepatitis virus (hepatitis C

    LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A
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100.0%; Pred. No. cc.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 884 from Patent WO9833904.
A88736
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Sequence 61 from Patent W09502051.
A42545
A42545.1 GI:2297994
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Pred. No. 85;
                                                                                                                                                                                                                                                                                                                               .. .15
'organism="unidentified"
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/db_xref="taxon:32644"
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1 (bases 1 to 14)
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Matches 11; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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BD263790 11-JUL-2003 AAeno-associated virus-delivered ribozyme compositions and methods
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Date in JP 2002542805-A 12 17-DEC-2002;
UNIVERSITY OF FLORIDA
OS Attificial Sequence
PP 12-002542805-A/12
PP 28-APR-2000 JP 2000515402
PR 28-APR-2000 JP 
                                                                                                                                                                                                                 artificial sequences.
1 (bases 1 to 15)
Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
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Patent: US 5610054-A 115 11-MAR-1997;
Location/Qualifiers
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    15 / Organism="synthetic construct"
/mol type="genomic RNA"
/db_xref="taxon:32630"

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Sequence 115 from patent US 5610054.
IS7578
IS7578.1 GI:2482642
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Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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BD263790.1 GI:33073558
JP 2002542805-A/12.
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1 (bases 1 to 15)
Draper, K.G.
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Unclassified.
1 (Dases 1 to 15)
1 (Dases 1 to 15)
Draper, K.G.
Method and reagent for inhibiting hepatitis C virus replication
Patent: US 586223-A 115 09-FBB-1999;
Location/Qualifiers
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Draper, K.G.
Method and reagent for inhibiting hepatitis C virus replication patent: US 6132966-A 115 17-OCT-2000;
Location/Qualifiers
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Pred. No. 85;
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Sequence 115 from patent US 6132966.
AR113171
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Sequence 115 from patent US 5869253.
AR033349.1 GI:5948954
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/organism="unknown"
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  Location/Qualifiers
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BD207082.1 G1:33016852

JP 2002512791-A/672.

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               PAT 15-DEC-2000
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Adeno-associated virus-delivered ribozyme compositions and methods
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 2; Indels
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/organism="synthetic construct"
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/db_xref="teaxon:32630"
/note="SYNTHETIC PEPTIDE"
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                RNA
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Haplotypes of the adrb3 gene
Patent: WO 0208425-A 19 31-JAN-2002;
Genalssance Pharmaceuticals, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                             Patent: WO 0066780-A 12 09-NOV-2000;
University of Florida (US)
Location/Qualifiers

    .15
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Sequence 19 from Patent WO0208425.
AX362585 AX362585.1 GI:18694729
          Sequence 12 from Patent WO0066780.
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Best Local Similarity 84.6
Matches 11; Conservative
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E Blatt.1. Mcswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
S Blatt.1. Mcswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
L Patent: JP 2002512791—A 672 08-MAY-2002;
RIBOZYME PHARMACEUTICALS ID.
OS HEPATITIS VIRUS (hepatitis C virus)
PN JP 2002512791—A/672
PP 26-APR-1999 UP 2000545991
PR 27-APR-1999 UP 2000545991
PR 27-APR-1999 US 60/08217,18-SEP-1999 US 09/274553 PI
LAWENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO.
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 2; Indels
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Method for determining homeostasis of the skin
Patent: WO 2023774-4 2992 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 2992 from Patent WO02053774.
AX625951
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
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PAT 20-APR-2002

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Unknow...
Unclassified.
1 (bases 1 to 12)
1 (bases 1 to 12)
Rothberg, J.Marc., Nallur, G.N. and Hu, X.
Rothberg, J.Marc., measuring differential gene expression
Methods and devices for measuring differential gene expression
Patent: US 6355423-8, 67 12-WAR-2002;
Location/Qualifiers
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1 (bases 1 to 12)
1 (bases 1 to 12)
Paparatus for determining DNA sequences by mass spectrometry
Patent: US 5174562-A 2 29-DEC-1992;
Location/Qualifiers
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Pred. No. 76;
0; Mismatches 1; Indels
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Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5569 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
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/organism="unknown"
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Sequence 67 from patent US 6355423.
AR199211. GI:20249285
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AR362486
AR362486.1 GI:34422687
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Matches 10; Conservative
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AR199211
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AR362486
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 64;
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Method for determining homeostasis of the skin
Patent: WO 2023774-8471 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 0205374-4 4953 11-UVL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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90.9%; Pred. No. 6%; ...
               11 bp DNi
Sequence 4953 from Patent WO02053774.
AX627912.
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Sequence 5471 from Patent WO02053774.
AX628430
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    .11
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/mol_type="unassigned DNA"
/db_xref="taxon;9606"

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Pred. No. 6
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Sequence 5569 from Patent
AX628528
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                                                                      AX627912.1 GI:28455950
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Matches 10; Conserv
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Best Local Similarity
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Matches

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ESULT 87 X628528/c OCUS

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PAT 05-DEC-1998

ESULT 90 R362486/c OCUS

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Unclassified.
Unclassified.
1 (bases 1 to 14)
Draper,K.G.
Method and reagent for inhibiting herpes simplex virus replication
Patent: US 6440719-A 20 27-AUG-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 14)
Draper, K.G.
Method and reagent for inhibiting herpes simplex virus replication
Patent: US 5795778-A 20 18-AUG-1998;
Location/Qualifiers
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Pred. No. 1.2e+02;
0; Mismatches 3; Indels
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               1 (bases 1 to 14)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION NETHOD
PALENT: WO 983304-A 983 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
                                                                                                                                                                                                       ch 32.9%; Score 9.2; DB 1; Similarity 78.6%; Pred. No. 1.2e+02; 11; Conservative 0; Mismatches 3
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AR224289
AR224289.1 GI:23333066

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/db_xref="taxon:32644"

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Sequence 20 from patent US 5795778.
AR024070. GI:3977364
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/organism="unknown"
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 78.6%;
Matches 11; Conservative
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AR024070/c
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AR224289/c
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Schlingensiepen, R., Schlingensiepen, K. and Brysch, W.
Brysch, W.
A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
PATENT K GES PURR BIOMOGEKUL (DE)
BIOGNOSTIK GES PURR BIOMOGEKUL (DE)
Other publication AU 7345594 950206.
                                                                   PAT 03-SEP-2003
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Brennan, T.M.
Apparatus for determining DNA sequences by mass spectrometry
Patent: US 5174962-A 2 29-DEC-1992;
Location/Qualifiers
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33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 1; Indels
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Sequence 164 from Patent WO9502051.
A42646
A42646.1 GI:2298095

    .14
/organism="unidentified"
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/db_xref="taxon:32644"

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                                                            12 bp
Sequence 2 from patent US 5174962.
AR362486
AR362486.1 GI:34422687
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/organism="unknown"
/mol_type="genomic DNA"
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C12N15/09, C12N5/10, C12N7/00, C12N9/22//(C12N5/10, C12R1:91),
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Pred. No. 1.2e+02;
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    ^2eganism="synthetic construct"
|mol_type="genomic RNA"
|db_xref="taxon:32630"

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1-MAY-1992 US 07/8826
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Best Local Similarity 78.6%;
Matches 11; Conservative
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artificial sequences.

1 (bases 1 to 14)
Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
Method eagent for inhibiting viral replication
Patent JP 2000342285-A 334 12-DEC-2000;
SARIATICIAL Sequence
SM Artificial Sequence
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Method and reagent for inhibiting HBV viral replication Patent: EP 1288256-A 352 05-MAR-2003;
RIBOZYME BHARMACEUTCALS, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .14
|organism="Herpes simplex virus unknown type"
|mol_type="unassigned RNA"
|db_xrefe"taxon:126283"
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Herpes simplex virus unknown type
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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Pred. No. 1.2e+02;
0; Mismatches 3; Indels
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11-MAY-1992 US
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PI JAMES J HOLESEK,ANTHONY J MAMONE
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Sequence 352 from Patent EP1288296.
AX711052
AX711052.1 GI:29787433
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BD001174.1 GI:18625733
JP 2000342285-A/334.
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Best Local Similarity 78.6%;
Matches 11; Conservative (
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16-AUG-1992 U
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PC A61R39/13, (C12N1-27) 125, A61R39/13, A61R39/245, A61R39/245, A61R39/29, A61R48/00, C12N15/09, C12R1:93) (C12N15/09, C12N15/09, C12N15/00, C12N15/3) (C12N15/3) (C
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C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
A61K39/145,
A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
A61P1/16,
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artificial sequences.
a third of the sequences artificial sequences.
braper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J. and Mamone, A.J.
Method and reagent for inhibiting viral replication
RIBOZYNE PHARMACEUTICALS INC
SATTLEGIAL Sequence
PN JP 2000342286-A, 334
PD 12-DEC-2000
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BD001603
Method and reagent for inhibiting viral replication.
BD001603.1
GI:18626162
JP 2000342286-A/334.
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Query Match 32.1%; Score 9; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 79; Matches 9; Conservative 0; Mismatches 0; Indels
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 14)

Schlingenslepen,K.H. and Brysch,W.
An antisense oligonucleotide preparation method
Patent: JP 2001511000-A 983 07-AUG-2001;
BICGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Uhknown
PN JP 2001511000-A/983
PN JP 20151000-A/983
PP 30-JAN-1997 EP 97101531.8
PR 31-JAN-1997 EP 97101531.8
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07-AUG-2001
30-JAN-1998 DP 1998532533
31-JAN-1997 EP 97101531.8
XARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRXSCH
C12115/11, C07121/04, AG1X31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels
                                                 Query Match
32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels
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An antisense oligonucleotide preparation method.
BD066348
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Patent: WO 0138577-A 29 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Location/Qualifiers
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Sequence 29 from Patent WO0138577.
AX152114

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JP 2001511000-A/983.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                               Length 10;
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Method for determining homeostasis of the skin
Petent: WO 2025374-A 5502 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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                                                                                                                                                                                                                                                                                                                       AX626581 11 bp DNA Sequence 3622 from Patent WO02053774.
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     PAT 07-MAR-1997
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Unknown.
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1 (bases 1 to 12)
Colote, S. and Pirotzky, E.
Colote, S. and Pirotzky, E.
Oligonucleotides to inhibit the expression of isoprenyl protein transferases
Fatent: US 5856461-A 6 05-JAN-1999;
Patent: US 5856461-A 6 05-JAN-1999;
Location/Qualifiers
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Oligonucleotides to inhibit the role of isoprenyl protein
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100.0%; Pred. No. 94;
iive 0; Mismatches
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ARQUENCE 6 from patent US 5856461.
AR027864 GI:5938684
12 bp
Sequence 6 from Patent EP0692535.
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
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PN 41792-8/7217
PD 10-D2C-2041795-8/7217
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/12399
PT 1AWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
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Rothberg,J.Marc., Nallur,G.N. and Hu,X.
Methods and devices for measuring differential gene expression
Patent: 18 6355423-A 67 12-MAR-2002;
Location/Qualifiers
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                                               DD259434.1 GI:33069194
DD259434.1 GI:33069194
UP 20025441795-A/7217.
Unidentified
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1 (base 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Repetati. JP 2002541795-A 7217 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
Regulation of repressor genes using nucleic acid molecules
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Inoue, K.

Method and device for amplifying DNA fragment

Datent: JP 200270867-A 211 03-OCT-2000;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
OS Unidentified
PN JP 2000270867-A/211
PD 03-OCT-2000
PF 19-MAR-1999 JP 1999076844
PR
PR COICHI INOUE
PC CLEANINGOUS CC Strandedness: Single;
CC Topology: Linear;
FT Source (organism='Unidentifiers)
FT Source (organism='Unidentified'.
                                                                                                                        Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of microorganism existing and method for estimating state of waste Patent: JP 199976176-A 211 12-CT-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES
ON UNIQUALIFIED
DN UP 1999276176-A/211
DP 12-OCT-1999
PP 31-MAR-1998 JP 1998087652
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PC C12N15/09, B09B3/00, C12Q1/00, C12Q1/68, C12N15/00, B09B3/00 CC
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Method and device for amplifying DNA fragment.
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83.3%; Pred. No. 1e+02;
tive 0; Mismatches

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JP 2000270867-A/211.
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E29731.1 GI:13021234
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1 (bases 1 to 12)
1 (bases 1 to 12)
NUCLEIC ACID MOLECULE ENCODING A (POLY) PEPTIDE CO-SEGREGATING IN
NUCLEIC ACID MOLECULE ENCODING POLYENDOCRINOPATHY CANDIDIASIS
ECTODERALD LYSTROPHY (APECED)
PARTEL TWO 9918197-A 4 15-APR-1999;
MAX PLANCK GESELLSCHAFT (DE), YASPO MARIE LAURE (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method of amplifying DNA fragment, apparatus for amplifying DNA fragment, method of assaying microorganisms, method of analyzing microorganisms and method of assaying contaminant Patent: US 6287769-A 211 11.8EP-2001; Location/Qualifiers
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31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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    .12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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/wol_type="unassigned DNA"
                                                                                                                      12 bp
Sequence 4 from Patent WO9918197.
A97287.1 GI:6780670
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1 (bases 1 to 12)
Inoue, T.
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                      12 GTACAGGTAGGC 1
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129731/c
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/mol_type="unassigned RNA"
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AR088591/c
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AR178839/c
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Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, method for analyzing a group of microorganisms, and method for analyzing substance.
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Unclassified.
1 (bases 1 to 13)
Faucher, C.R.J.
Fixing unit with an end imprint in a threaded terminal portion
Fatent: US 6632057-A 30 14-OCT-2003;
Location/Qualifiers
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Location/Qualifiers
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Pred. No. 1e+02;
0; Mismatches 2; Indels
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/organism="synthetic construct"
/mol_typc="genomic DNA"
/db_xref="taxon:32630"
     Pred. No. 1e+02;
0; Mismatches
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JP 1999341989-A/211.
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artificial sequences.
1 (bases 1 to 12)
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83.38;
     83.3%;
Best Local Similarity 83.3
Matches 10; Conservative
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Bennett, C.Frank. and Vickers, T.A.
Bennett, C.Frank. and Vickers, T.A.
Oligonuclectide compositions and methods for the modulation of the expression of B7 protein
expression of B7 protein
Patent: US 6077833-A 85 20-UJN-2000;
Location/Qualifiers
                                        Gaps
                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 10)
Thompson, J.D.
Method and reagent for inhibiting P-glycoprotein (mdr-1-gene)
Patent: US 598996-A, 7 23-NOV-1999;
Location/Qualifiers
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 Length 13;
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 Score 8.8; DB 1; Length 13
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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Pred. No. 89;
0; Mismatches
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/organism="unknown"
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/wol_type="unassigned DNA"
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ARI78839
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Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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Jnclassified.
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Gaps

AR178839.1 GI:20219977

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PAT 22-JUN-2001
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams, E., Waldmann, H., Cobbold, S. and Zelenika, D.
Genes differentially expressed in trl cells and their use in the
manufacture of immunoregulatory compositions
Patent: WO 0127267-A 71 19-APR-2001,
ISIS INNOVATION LIMITED (GB)
Location/Qualifiers
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             1 (bases 1 to 10)
Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
Androgen-regulated gene expressed in prostate tissue
Patent: US 6566130-A 14 20-WAY-2003;
Location/Qualifiers
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Pred. No. 89;
0; Mismatches 1; Indels
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Pred. No. 89;
0; Mismatches 1; Indels
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Patent: WO 0138577-A 1257 31-MAY-2001;
The John Hopkins University (US)
Location/Qualifiers
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Sequence 1257 from Patent WO0138577.
AX153342.1 GI:14534993
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/organism="Mus sp:"、
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                       AX113024 10 bp
Sequence 71 from Patent WO0127267.
AX113024
                                                                                                                           /organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 90.0%;
Matches 9; Conservative
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AX113024/c
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J P 20012183-4/4.

Homo sapiens (human)

B 1 (bases 1 to 10)

S Mateushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human normal liver cell expression genes

L Patent: JP 2001211883-4 4 07-AUG-2001;

SCIENCE & TECH AGENCY

OS Homo sapiens (human)

PN JP 20012211883-A/4
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                                         Unknown.
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1 (bases 1 to 10)
1 (bases 1 to 20)
1 Semmetr, C. Frank.
Dennett, C. Frank.
Oligonucleotide compositions and methods for the modulation of the expression of B7 protein
expression of B7 protein
Patent: US 6319906-A 85 20-NOV-2001;
Location/Qualifiers
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10 GGGAGGCCAG 1

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/organism="unidentified"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
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1 (bases 1 to 10)
Matsushima, K., Hashimoto, S., Kaneko, S. and
Matsushima, K., Hashimoto, S., Kaneko, S. and
Human liver disease-expressing genes
Patent: JP 2002209591-A 328 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Home agaiens (human)
PN JP 2002209591-A/328
PD 30-JUL-2002
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Key
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Haplotypes of the ntf3 gene
Patent: WO 0212499.A 20 14-FEB-2002;
Genaissance Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 20 from Patent WO0212499.
AX377356
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JP 2002209591-A/328.
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Numan liver disease-expressing genes.

Numan liver disease-expressing genes.

BD167059.1 GI:27872871

DP 2002209591-A/604.

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BUKATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(base 1 to 11)
Landers 1.E., Jordan, B., Housman, D.E. and Charest, A. Methods and products related to genotyping and DNA analysis Patent: JP 200255127-A 5 13-AUG-2002; MASSACHUSETTS INSTITUTE OF TECHNOLOGY

S Home sapiens (human)
PN J 2002525127-A/5
PD 13-AUG-2002
PF 24-SEP-1999 US 60/101757
PR 25-SEP-1999 US 60/101757
PR JS-EP-1999 US 60/101757
PR JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSWAN, ALAIN CHAREST PC
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              Unknown.
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Unclassified.
I bases.
Bennett, C.Frank. and Vickers, T.A.
Oligonucleotide compositions and methods for the modulation of the expression of B7 protein
Patent: US 607783.A 86 20-JUN-2000;
Location/Qualifiers
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1 (bases 1 to 11)

1 (bases 1 to 11)

Shapesty, C.Frank. and Vickers, T.A.
Oligonuclectide compositions and methods for the modulation of the expression of B7 protein
Patent: US 6319906-A 86 20-NOV-2001;
Location/Qualifiers
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Sequence 86 from patent US 6319906.
AR178840.1 GI:20219978
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JP 2002525127-A/5.
Homo sapiens (human)
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C12P21/08,
                       C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02, C12P21/08, C12P15/00
C12N15/00
Luman liver disease-expressing genes Location/Qualifiers
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BD167159.1 GI:27872970

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E 2002209591-A 703 30-UUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/703

PD 30-UUL-2002

PF 19-JAN-2001 JP 2001012328

PI 4031 MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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Location/Qualifiers
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Location/Qualifiers
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Sequence 86 from patent US 6077833.
AR099559
AR099559.1 GI:12809325
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30.0%; Score 8.4; DB
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches

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PC C12N1
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RESULT 124 AR099559/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS

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Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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AX470626/c
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Methods and products related to genotyping and DNA analysis FH
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Polymorphisms in the human hpxr gene and their use in diagnostic and therapeutic applications
Patent: WO 0120026-A 106 22-MAR-2001;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
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                                                                              /organism='Homo sapiens (human)'. Location/Qualifiers
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Patent: US 6538173-A 45 25-WAR-2003;
Location/Qualifiers
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Sequence 106 from Patent W00120026.
AX099043.1 GI:13538253
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Sequence 45 from patent US 6538173.
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AR301464.1 GI:31689266
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Best Local Similarity 90.0"
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Heber-Katz, E.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Polymorphisms in the human hpxr gene and their use in diagnostic and therapeutic applications
Patent: WO 0120026-A 107 22-MAR-2001;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: W0 02053773-A 203 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Score 8.4; DB 1; Length 11;
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                                                0; Mismatches
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Sequence 107 from Patent WO0120026.
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PAT 09-AUG-2002

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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Identification of the genetic determinants of the polymorphic cypals expression
Patent: WO 02083775-A 89 11-JUL-2002;
PRIDAUROS BIOTECHNOLOGIE AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 770 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 430 11-JUL-2002;
HENKEL KGAA (DE)
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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Seguence 770 from Patent WO02053773.
AX471193
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Sequence 89 from Patent WO02053775.

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AX472098.1 GI:22207139
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Matches 9; Conservative
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Homo sapiens
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 334 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
                                                                                                                                                                                                               Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 222 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Sequence 430 from Patent WO02053773.
AX470853
                Sequence 222 from Patent WO02053773.
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Homo sapiens
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Best Local Similarity 90.0
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 958 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                   Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 2005374-4-705 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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AX623664 11 bp DNA Sequence 705 from Patent WO02053774. AX623664 1 GI:28451605
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Sequence 958 from Patent WO02053774.
AX623917

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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  Score 8.4; DB 1; Length 11; Pred. No. 1.18+02; 0; Mismatches 1; Indels
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Sequence 411 from Patent WO02053774.
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Sequence 373 from Patent WO02053774.
AX623332
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AX623370.1 GI:28451311
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Petersohn, D., Conradt, M. and Hofmann, K.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AX627101.1 GI:28455139
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DEFINITION Sequence 6225 from Patent WO02053774.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 1993 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2263 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
Method for determining homeostasis of the skin
Patent: WO 02053774-4, 1072 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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AX625222.1 GI:28453163
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AX624952.1 GI:28452893
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Sequence 7832 from Patent WO02053774.
Ax630791
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Sequence 7794 from Patent WO02053774.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                       Eukaryoča, Metazoa, Chordata, Craniata, Vertebzata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 6225 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 7017 from Patent W002053774.
AX629976.1 GI:28458014

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-4,9685 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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90.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 1;
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WO02053774.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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  GGGAGTCCAG 27
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 11)
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Patent: JP 2012503460-A 45 05-FEB-2002;
PHE MISTAR INSTITUTE
OS Mus musculius (mouse)
PD 05-FEB-1090
PD 05-FEB-1090
PD 12-FEB-1999 JP 2000531545
PR 13-FEB-1999 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1996 US 60/102051
PI ELLEN HEBER KATZ
PC CLINIS/09, A01K67/027, CLINIS/10, ISONO 1800 MISS 1800 
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/organism='Mus musculus (mouse)'.
Location/Qualifiers
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Patent: EP 0692535-A 28 17-JAN-1996;
'organism="Homo sapiens"
'mol_type="unassigned DNA"
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Sequence 28 from Patent EP0692535.
A47668.1 GI:2301609

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1 (bases 1 to 12)
Colote, S. and Pirotzky, E.
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JP 2002503460-A/45.
Mus musculus (house mouse)
Mus musculus
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Unknown.
Unclassified.
1 (bases 1 to 12)
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Draper,K.G.
Method and reagent for inhibiting herpes simplex virus replication
Patent: US 5795778-A 39 18-AUG-1998;
Location/Qualifiers
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Colote,S. and Pirotzky,E.
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721239 960328
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Sequence 28 from patent US 5856461.
AR027886
AR027886.1 GI:5938706
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Other publication CA 215233 951230
Other publication GB 2290791 960110
Location/Qualifiers
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AR024089
AR024089.1 GI:3977383
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JP 2002534966-A/25.
Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 12)
Bennett,(-7. Frank. and Vickers, T.A.
Olispanucleotide compositions and methods for the modulation of the expression of B7 protein
Patent: US 6077833-A 87 20-JUN-2000;
Patent: US 6077833-A 87 20-JUN-2000;
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Unclassified.
In (bases 1 to 12)
I (bases 1 to 12)
Inoue, T.
Method of amplifying DNA fragment, apparatus for amplifying DNA fragment, method of assaying microorganisms, method of assaying microorganisms and method of assaying contaminant
Patent: US 6287769-A 107 11-SEP-2001;
Location/Qualifiers
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30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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Patent: US 5856461-A 28 05-JAN-1999;
Location/Qualifiers
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Sequence 87 from patent US 6077833.
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/organism="unknown"
/mol_type="unassigned DNA"
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PAT 20-APR-2002
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Bennett, C.Frank. and Vickers, T.A.
Bennett, C.Frank. and Vickers, T.A.
Oligonuclectide compositions and methods for the modulation of the expression of B7 protein
Patent: US 6319906-A P7 20-NOV-2001,
Location/Qualifiers
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Cramari,A., Stemmer N.P.C., Minshull,J., Bass,S.H., Welch,M., Ness,J.E., Gustafsson,C. and Patten,P.A.
                                                                                                                                                                                 Unclassified.

1 (bases 1 to 12)
Crameri, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M., Crameri, A., Guttefsson, C. and Patten, P.A.
Oligonucleotide mediated nucleic acid recombination
Patent: US 6319714-A 25 20-NOV-2001;
Location/Qualifiers
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BD251252
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linear
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TITLE JOURNAL

MMENT

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Induce, N.

Method and device for amplifying DNA fragment
Patent: JP 200270867-A 107 03-OCT-2000;
SANYO ELECTRIC CO LID, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
PRESTRY AND FISHBRIES
OS Unidentified
PN JP 200270867-A/107
PD 03-OCT-2000
PR 19-MAR-1999 JP 1999076844
PR 19-MAR-1999 JP 1999076844
PR CIZINIS/00
CC Strandedness: Single;
CC Topology: Linear;
FT source

| Location/Qualifiers
| Location/Qualifiers
| Location/Qualifiers
| Location/Press: Vinidentified
| Location/Qualifiers
| Location/Press: Vinidentified
| Location/Press: Vi
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E64159. [GI13019563]
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We thod for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substance
Patent: JP 1999341989-A 107 14-DEC-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FIRBRIES
OS ARLIficial Sequence
NO JP 1999341989-A/107
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Method and device for amplifying DNA fragment.
E38733
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Location/Qualifiers
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90.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 1.
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/organism="unidentified"
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/db_xref="taxon:32644"
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JP 2000270867-A/107.
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1 (bases 1 to 12)
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                                           7 CTACGIGIAC 16
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Matches 9; Conserv
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E64159/c
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Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste microorganism existing and method for estimating state of waste patent: JP 1999276176-A 107 12-OCT-1999;
SANYO BLECTRIC CO LID, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FILES
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CC C12N5/00
CC Oligonucleotide mediared modiared modiared modiared modiared
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PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
Strandedness: Single;
Location/Qualifiers
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60/141049 PR
09/408393 PR
09/416837 PI
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05-FEB-1999 US 60/118854,24-UUN-1999 US 60/141049 PR
05-FEB-1999 US 60/440839,28-SEP-1999 US 60/440839 PR
12-OCT-1999 US 09/448375,12-OCT-1999 US 09/416837 PI
ANDREAS CRAMERI,WILLEM P C STEMMER, JEREMY MINSHULL, STEVEN H
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Oligonucleotide mediated nucleic acid recombination
Patent: JP 2002534966-A 25 22-OCT-2002;
MAXYGEN INC
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Location/Qualifiers

    .12
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Location/Qualifiers
                                                                                                                                                                                 PD 22-0CT-2002
PF 18-JAN-2000 JP 2000594068
PR 19-JAN-1999 US 60/11644
05-FEB-1999 US 60/118854,28-
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JP 1999276176-A/107
12-OCT-1999
                                                                                                                  Homo sapiens (human)
JP 2002534966-A/25
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JP 199276176-A/107.
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Best Local Similarity 90.v.
Best Local 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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PAT 20-DEC-2002
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Draper, K.G.
Method and reagent for inhibiting herpes simplex virus replication Patent: US 6440719-A 39 27-AUG-2002;
Location/Qualifiers
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Crameri, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M., Ness, J.E., Gustafsson, C. and Patten, P.A.
Oligonucleotide mediated nucleic acid recombination
Patent: US 642624-A 25 30-JUL-2002;
Location/Qualifiers
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Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.3e+02;
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Sequence 25 from patent US 6479652.
AR254226
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Sequence 25 from patent US 6426224.
AR221524.
AR221524.1 GI:23328574
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Sequence 39 from patent US 6440719.
AR224308.1 GI:23333085
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/organism="unknown"
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Matches 9; Conservative
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AR254226
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AR224308
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AR221524
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Unclassified.

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I (bases 1 to 12)
Cramer, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M., Ness, J.E., Gustafsson, C. and Patten, P.A.
Ness, J.E., Gustafsson, C. and Patten, P.A.
Oligonucleotide mediated nucleic acid recombination
Patent: US 636861-A 25 09-APR-2002;
Location/Qualifiers
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Unclassified.
Unclassified.

1 (bases 1 to 12)
Cramer, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M., Ness, J.E., Quetafson, C. and Patten, P.A.
Oligomucleotide mediated nucleic acid recombination
Patent: US 6423542-A 25 23-JUL-2002;
Location/Qualifiers
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/organism='Artificial Sequence'
Location/Qualifiers
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30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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C12N15/09,C12M1/00,C12Q1/68,C12N15/00
                                                                                                     Location/Qualifiers

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        /organism="synthetic construct" | mol_type="genomic DNA" | db_xref="taxon:32630"

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Sequence 25 from patent US 6423542.
AR220135
AR220135.1 GI:23324577
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/mol_type="unassigned DNA"
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Sequence 25 from patent US 6368861.
AR205443.1 GI:21503026
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      14-DEC-1999
16-MAR-1999 JP 1999069694
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Best Local Similarity 90.0
Matches 9; Conservative
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Method and reagent for inhibiting HBV viral replication Patent: EP 1288296-A 390 05-MAR-2003;
RIBOZYME PARRACEUTICALS, INC. (US)
Location/Qualifiers
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Herpes simplex virus unknown type
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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llarity 90.0%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 1
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/db_xref="taxon:32630"
0; Mismatches
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Sequence 390 from Patent EP1288296.
AX711090
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Sequence 4 from Patent W00250108.
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synthetic construct
artificial sequences.
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BD001193
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Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
Oligonucleotide mediated nucleic acid recombination
Patent: US 6376246-A. 25 23.APR-2002;
Location/Qualifiers
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Crameri, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M., Ness, J.E., Gustafsson, C. and Patten, P.A.
Oligonucloetide mediated nucleic acid recombination
Patent: US 5521453-A 25 18-FEB-2003;
Location/Qualifiers
                                                 Crameri, A., Stemmer, W.P.C., Minshull, J., Bass, S.H., Welch, M., Ness, J.E., Gustafsson, C. and Patten, P.A.
Oligonucleotide mediated nucleic acid recombination
Patent: US 6479652-A 25 12-NOV-2002;
Location/Qualifiers
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llarity 90.0%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 1.
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Sequence 25 from patent US 6376246.
AR368339
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Sequence 25 from patent US 6521453.
AR282432
AR282432:1 GI:29718588
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./organism="unknown"
./mol_type="genomic DNA"
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/organism="unknown"
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Best Local Similarity 90.0%;
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C12N15/09, C12N5/10, C12N7/00, C12N9/22//(C12N5/10, C12R1:91), PC
             ## BD001193.1 GI:18625752
## Synchetic construct
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JP 2000342286-A/33.
Synthetic construct
synthetic construct
artificial sequences.
I (bases 1 to 10)
S Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J. and Mamone, A.J.
Method and reagent for inhibiting viral replication
RIBOZYME HARMACEUTICALS INC
OR Artificial Sequence
PN JP 2000342286-A/353
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Location/Qualifiers
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Method and reagent for inhibiting viral replication.
BD001622
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Pred. No. 1.3e+02;
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PC A61K39/23, A61K39/245, A61K39/245, A61K39/13, (C12N15/09, A61K48/00, A61K31/14, A61P31/16, A61P31/18, A61E31/22, A61E35/02, C12Q1/68, PC C12R1:93) (C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC CC PH Key Location/Qualift
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CI2NIS/09,CI2NS/10,CI2N7/00//A61K38/43,A61K39/125,A61K39/13,
A61K39/135,
A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
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    12
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| Hilton, D.James.
| Holl ton terleukin-11 receptor
| Patent: US 6274708-A 19 14-AUG-2001;
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Sequence 19 from patent US 6274708.
AR165205
AR165205.1 GI:16238680
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JP 2000132651
US 07/8826
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Best Local Similarity 76.9
Matches 10; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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PI JAMES
PC C12N;
PC A61K;
PC A61K;
PC A61P;
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                           PAT 06-JUL-2002
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Position dependent recognition of gnn nucleotide triplets by zinc
                                                                                                         Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Similarity 100.0%; Pred. No. 8.1e+02;
8; Conservative 0; Mismatches 0;
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                                                                                                                                                                       Kurreck,J. and Erdmann,V.A.
Antisense oligonucleotides against vr1
Patent: WO 0218407-A 97 07-MAR-2002;
Gruenenthal GmbH (DE)
Location/Qualifiers
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Patent: WO 0242459-A 2098 30-MAY-2002;
Sangamo Blosciences Inc. (US)
Location/Qualifiers
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Sequence 2100 from Patent W00242459.
AX668651.1 GI:29291626
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Sequence 2098 from Patent WOO242459.
AX668649
                         9 bp
Sequence 97 from Patent WO0218407.
AX456625
                                                                                           Rattus norvegicus (Norway rat)
                                                                AX456625.1 GI:21715512
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Liu,Q.
Position dependent recognition of gnn nucleotide triplets by zinc fingers: WO 0242459-A 2100 30-MAY-2002;
Patent: WO 0242459-A 2100 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Position dependent recognition of gnn nucleotide triplets by zinc
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Patent: WO 0242459-A 2453 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Fatent: WO 0242459-A 2195 30-MAY-2002;
Sangamo Biosziences Inc. (US)
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Sequence 2195 from Patent WO0242459.
AX668746
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BD240218
LOCUS
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AUTHORS
TITLE
JOURNAL
                                                                                   RESULT 186
                                                                                                           BD238631
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Position dependent recognition of gnn nucleotide triplets by zinc
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28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      0; Indels
                                                                                                                                    Length 9;
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100.0%; Pred. No. 8.1e+02;
tive 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Patent: WO 0242459-A 2454 30-MAY-2002;
Sangamo Biostiences Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           AX669005
Sequence 2454 from Patent WO0242459.
AX669005

    .10
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260uence 12 from Patent EP0561245.
A78814
A78814.1 GI:6090408
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synthetic construct
artificial sequences.
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
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   PAT 17-JUL-2003
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JP 2002534056-A/1636.
Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Cases 1 to 10)

Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 202534056-A 49 15-OCT-2002;
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60/090921,19-UTN-1998 US
60/099921,19-UTN-1998 US
60/099991,19-UTN-1998 US
60/099991,19-UTN-1998 US
60/09000119-UTN-1998 US
60/0900042,19-UTN-1998 US
60/090042,19-UTN-1998 US
60/090081,19-UTN-1998 US
60/090981,19-UTN-1998 US
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19-JUN-1998 US 60/0900
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JP 2002534056-A/49
15-OCT-2002
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Homo sapiens (human)
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PN JF
PD 07
PF 31
PI KC
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PI LYI
C12N15/
CC Mi
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DEFINITION
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DEFINITION
ACCESSION
VERSION
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SOURCE
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E54660
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G01N37/00,
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COMMISSARIAT A L'ENERGIE ATOMIQUE, CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 10)

Roberts, B.L. and Shankara, S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 1636 15-OCT-2002;

GENZYME CORP
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60/089993
60/089991
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C12N15/00,C12N5/00,C12N15/00
Preparation and use of superior vaccines
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60/089927.19-UN-1998 US
60/089927.19-UN-1998 US
60/089928.19-UN-1998 US
60/0899818.19-UN-1998 US
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60/080042.19-UN-1998 US
60/080044.19-UN-1998 US
60/089994.19-UN-1998 US
60/089994.19-UN-1998 US
60/080080.19-UN-1998 US
60/080080.19-UN-1998 US
60/080080.19-UN-1998 US
60/080078.19-UN-1998 US
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60 (099992, 19-0TN-1998 U

60 (090042, 19-0TN-1998 U

60 (090041, 19-0TN-1998 U

60 (090080, 19-0TN-1998 U

60 (0909994, 19-0TN-1998 U
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Best Local Similarity 100.0%; Pred. No. 1.:
Matches 8; Conservative 0; Mismatches
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JP 2002535012-A/11
22-OCT-2002
25-JAN-2000 JP 2000596176
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|8-JUN-1999 JP 2000554749
|9-JUN-1998 US 60/09003
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                                                                                           Homo sapiens (human)
JP 2002534056-A/1636
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JP 2002535012-A/11.
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D242821/c
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27-JAN-1999 EP 99400189.9
LYDIE CHEYNL, JEAN MARC ELALOUF, BERANGERE VIRLON PC
15/09, C12Q1/68, C12U15/00
Microassay for continuous analysis of gene expression and its
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28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                  (mouse)'.
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                                                                    Location/Qualifiers
                                                                                       rce 1. .10
/organism='Mus sp.
Location/Qualifiers
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Sequence 12 from patent US 5661124.
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                                                                                                                                                                                                      28.6%; Score 8; 100.0%; Pred. No.

    10
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    /mol_type="genomic DNA"
    /db_xref="taxon:10095"

                                                        application
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JP 2001211883-A/12.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                            Krieg, A.M., Schetter, C. and Vollmer, J.C.
Immunostimulatory nucleic acids
Batent: WO 0122972-A 1125 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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    ^ 10
    ^ 0xganism="synthetic construct"
    ^ mol_type="unassigned DNA"
    ^ db_xref="taxon:32630"

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llarity 100.0%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 0;
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AX104933
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Sequence 464 from Patent WO0138577.
AX152549
AX152549.1 GI:14534200
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Unclassified.
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Unclassified.
Cheval, L., Elalouf, J.-M. and Virlon, B.
Method of obtaining a library of tags capable of defining a specific state of a biological sample patent: US 6506561-A 12 14-JAN-2003;

Location/Qualifiers
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Location/Qualifiers

Location/Qualifiers

/ And type="unassigned DNA"

/ db_xref="taxon:10095"
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28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 10)
Hoffman, S. J. and Nagai, K.
Blood substitutes
Patent: US 5661124-A 12 26-AUG-1997;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo.

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Matsushima, K., Hashimoto, S. and Suzuki, T.

LPS activated human monocyte expressing genes patent: 19 2001069993-A 169 21-MAR-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

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PP 28-APR-2000 JP 2000131079
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CIZNIS/09,CO7K14/47,CO7K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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JP 20101069993-A/169. Homo sapiens (human) Homo sapiens (human) Bukaruche.
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/db_xref="taxon:9606"
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20guence 53 from Patent WO0210454.
AX374632 AX374632.1 GI:19169529
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0185941-A 372 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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Patent: WO 0138677-A 936 31-WAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                           Velculescu,V.E., Vogelstein,B. and Kinzler,K.W. Human transcriptomes
Patent: WO 0138577-A 674 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 936 from Patent WO0138577.
AX153021
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Sequence 372 from Patent WO0185941.
AX301658
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        AX152759.1 GI:14534410
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JP 2001327293-A/244.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 8; Conservative
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M. (Dasea: 1 to 10.)

Matsushima, K., Hashimoto, S. and Suzuki, T.

LPS activated human monocyte expressing genes patent: 19 2001069993-A 197 21-MAR-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PD 31-MAR-2001

PD 21-MAR-2001

PP 28-APR-2000 JP 2000131079
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BD065573.1 GI:22610876
JP 2001509017-74/209.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Bukaryota, Fungi, Ascomycota; Saccharomycetine; Saccharomycetoles; Saccharomycetoles; Incertales; Saccharomycetoles; Ito 10)
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                 'organism='Homo sapiens (human)'.
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BD007921
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Characterization of the yeast transcriptome.
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100.0%; Pred. No. 1.1
cive. 0; Mismatches
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A61P31/00,C12P21/08,C12N15/00

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    .10
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                             Location/Qualifiers
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JP 2001069993-A/197.
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Characterization of the yeast transcriptome

Characterization of the yeast transcriptome

LPE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
N JP 2001509017-A/209
PD 10-UL-2001
PP 22-JAN-1998 JP 1998532117
PP 22-JAN-1998 US 60/035917
PI VICTOR E VELCULESCUY BERY VOGELSTEIN, KENNETH W KINZLER PC C12N15/10, C12N15/31, C70XX44/395, C1201/68, C1201/02 CC Characterization of the yeast transcriptome
FH Key Loure Longer 
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100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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AX421267
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AR282864
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TITLE
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                       BD167068.1 GI:27872880
BD167068.1 GI:27872880
Unidentified
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SM unidentified
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SM watcushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
Human liver disease-expressing genes
D Patent: JP 2002205591-A 613 30-UL-2002;
UAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002205591-A/613
PN JP 2002205591-A/613
PN JP 30-ULL-2002
PP 19-JAN-2001 JP 2001012328
PF 19-JAN-2001 JP 2001012328
PF SOURT STANERO, TARO PI
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C12P21/08,
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OS Home sapiens (human)

PN JP 2002209591-A/715

PP 19-JNA-2001

PP 201012328

PI 19-JNA-2001 JP 2001012328

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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Human liver disease-expressing genes
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Human liver disease-expressing genes
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BD167170
BD167170. GI:27872982
JP 2002209591-A/715.
   Human liver disease-expressing genes.
BD167068

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PC C12N1
PC C12P2
PC C12N1
CC Human
CH Key
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(bases 1 to 11)

(Enemer, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.

Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined
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28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                              0; Indels
28.6%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.18+02; ive 0; Mismatches 0; Indels
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Patent: US 6524792-A 9 25-FEB-2003;
Location/Qualifiers
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Sequence 40 from Patent WO0210217.
AX393110
AX393110.1 GI:19701160
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ARQUENCE 9 from patent US 6524792.
AR282864 GI:29719666

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AX470933/c
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AX470788
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    PAT 18-JUN-2002
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/note="Oligonucleotide of the novel polymorphic site 461
on the non-coding strand"
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1. 11
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/nofe="foligoncleotide of the novel polymorphic site 461
on the coding strand"
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0218641-A 16 07-MAR-2002;
Gemini Genomics PLC (GB)
Location/Qualifiers
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Patent: WO 0218641-A 15 07-WAR-2002;
Gemini Genomics Pic (GB)
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28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Sequence 46 from Patent WO02053773.
AX470469
11 bp
Sequence 15 from Patent WO0218641.
AX421267
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AX421268
                                                AX421267.1 GI:21524675
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artificial sequences.
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synthetic construct
artificial sequences.
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X421268/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent, WO 02053773-A 46 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 365 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 510 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Seguence 365 from Patent WO02053773.
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AX470933.1 GI:22206058
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AX470788.1 GI:22205913
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Best Local Similarity 100.0
Matches 8; Conservative
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PAT 21-FEB-2003
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 596 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                                     Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 101 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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AX624143
AX624143.1 GI:28452084
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11 bp DN Sequence 101 from Patent WO02053774. AX6230660 AX623060.1 GI:28451001
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Seguence 596 from Patent WO02053774.
AX623555
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1428 11-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 940 11-JUL-2002;
HENKEL KGAA (DE)
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28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
        Query Match

28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Sequence 1428 from Patent WO02053773.
AX471851 GI:22206976
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Location/Qualifiers

ATURES

AX471363 AX471363.1 GI:22206488

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SULT 212 471363

Homo sapiens (human)

Homo sapiens

URCE ORGANISM

FERENCE AUTHORS TITLE JOURNAL

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1. .11 /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="taxon:9606"

Query Match
Best Local Similarity 100.
Matches 8, Conservative

ESULT 214 K623060

Location/Qualifiers

HENKEL KGAA (DE)

SFERENCE AUTHORS TITLE JOURNAL

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Homo sapiens (human) Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AX625855
LOCUS AX625855 11 bp DNA-
DEFINITION Sequence 2896 from Patent WO02053774.
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Sequence 2491 from Patent WO02053774.
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  Mismatches
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AX625464.1 GI:28453405
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AX625464/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2179 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
Method for determining homeostasis of the skin
Patent: WO 02053774 + 1184 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0;
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Sequence 2229 from Patent W002053774.
AX625188.1 GI:28453129
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 8; Conservative 0; Mismatches 0; Indels
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Sequence 4823 from Patent WO02053774.
AX627782
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Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                  Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 2896 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 4054 from Patent WO02053774.
AX627013
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Sequence 3705 from Patent WO02053774.
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                               Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 20053774-A 7522 11-JUL-2002; Henkel Kommanditgeeellschaft auf Aktien (DE) Location/Qualifiers
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Method for determining homeostasis of the skin
Retnnt: WO 2020374-A 8606 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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AX631564.1 GI:28459640
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Sequence 8017 from Patent WO02053774.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0;
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Matches 8; Conservative 0; Mismatches 0;
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Sequence 6784 from Patent W002053774.
AX629743
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Libjatois, P., Loison, G., Pessegue, B. and Shire, D.
Artificial promoter for the expression of proteins in yeast
Patent: US 5407822-A 4 18-APR-1995;
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Sequence 4 from Patent US 5407822.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 9601 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for inhibiting HBV viral replication tentent: EP 128296-A 482 OB-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
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                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
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Seguence 482 from Patent EP1288296.
AX711182
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Sequence 89 from Patent WO02053775.
AX472098
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synthetic construct
artificial sequences.
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Best Local Similarity 100.
Matches 8; Conservative
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AX711182
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AX625951
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Hordeum vulgare
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum.
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Blaiseu, P.-L., Legoux, R., Leguay, J.-J. and Schneider, M. Recombinant DNA coding for a protein with endochitinase activity Patent: US 5446138-A 17 29-AUG-1995; Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 0;
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Unclassified.
3 | (bases 1 to 12)
5 Baxter-Lowe, L. Ann.
Method for HLA Typing
AL Patent: US 554526-A 15 13-AUG-1996;
Location/Qualifiers
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Sequence 15 from patent US 5545526.
124587.
124587.1 GI:1604457
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Sequence 23 from Patent WO0162967.
AX235321
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PAT 09-AUG-2002
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A, 324 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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1 (bases 1 to 11)

Hebber-Katz, E.

Compositions and methods for wound healing

Patent: US 6538173-A 272 25-MAR-2003;

Location/Qualifiers
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AX470906/c
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AR301691/c
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Weiss,A. and Fraser,J.
Screening assay for the identification ov novel immunosuppressives using cultured T cells
Patent: US 5474897-A 4 12-DEC-1995;
                                                                      Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Identification of the genetic determinants of the polymorphic cyp3a5 expression
Patent: WO 0207575-A 89 11-JUL-2002;
EPIDAUROS BIOTECHNOLOGIE AG (DE)
Location/Qualifiers
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27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Heber-Katz, B.
Compositions and methods for wound healing
Patent: US 658173-A 236 25-WAR-2003;
Location/Qualifiers
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Sequence 236 from patent US 6538173.
AR301655
AR301655.1 GI:31689457
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2000ence 4 from patent US 5474897.
116095.1 GI:1251003
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 AX472098.1 GI:22207139
                                     Homo sapiens (human)
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SFERENCE AUTHORS TITLE JOURNAL

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Gaps

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Patent: WO 02053773-A 1101 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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AX471669/c
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AX471699/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 483 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 529 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Sequence 529 from Patent WO02053773.
AX470952
    Sequence 483 from Patent WO02053773
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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AX470906.1 GI:22206031
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1246 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1276 11-JUL-2002;
HENKEL KGAA (DE)
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0; Mismatches 2;
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Sequence 1276 from Patent W002053773.
AX471699
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 0205374.4.1371 11.JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                               Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 1065 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 1878 from Patent WO02053774.
AX624837
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX624024.1 GI:28451965
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1373 11-JUL-2002;
HENKEL KGAA (DE)
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Sequence 1065 from Patent WO02053774.
AX624024
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Sequence 681 from Patent WO02053774.
AX623640.1 GI:28451581

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/db_xref="taxon:9606"

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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Homo sapiens
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Homo sapiens
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1 AGGAGACCTG 11

11. .11
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 /mol\_type="unassigned DNA"
 /db\_xref="taxon:9606"

9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

18 GGGAGTCCAGG 28

11 GGGAATACAGG 1

Location/Qualifiers

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AX625047 11 bp DNi Sequence 2088 from Patent W002053774. AX625047

AX625047.1 GI:28452988 Homo sapiens (human)

ESULT 255 X625047/C OCCS EFINITION CCESSION ERSION ERSION EVANCE OURCE ORGANISM

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                   AX625794 11 bp DNA Sequence 2835 from Patent WO02053774. AX625794
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                       27.9%; Score 7.8; DB 1; Length 11;
81.8%; Pred. No. 1.5e+02;
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1. .11 /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="taxon:9606"

source

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18 GGGAGTCCAGG 28

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11 GGTAGGCCAGG 1

AX625403 Sequence 2444 from Patent W002033774. AX625403 AX625403.1 GI:28453344

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1. .11 /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="taxon:9606"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.5e+02;
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Sequence 5006 from Patent WO02053774.
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Sequence 4701 from Patent W002053774.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 2023774-43 3929 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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                                                                                                 Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 3793 11-dUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 3929 from Patent WO02053774.
AX626888
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Sequence 3824 from Patent WO02053774.
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Best Local Similarity 81.8%;
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Homo sapiens
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Matches 9; Conservative
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Sequence 6246 from Patent W002053774.
AX629205
AX629205.1 GI:28457243
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Sequence 6612 from Patent WO02053774.
AX629571
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Best Local Similarity 81.8%;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 5562 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                   Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 5162 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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                      AX628121 11 bp DNA
Sequence 5162 from Patent WO02053774.
AX628121
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                         Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 7320 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Sequence 7320 from Patent WO02053774.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 6923 from Patent WO02053774.
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AX629882.1 GI:28457920
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Compositions and method for healing wound.

BD124405
BD124405.1 GI:23219350
JP 2002503460-A/236.
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
In karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 11)
Matz, E.H.
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C12N15/09, A01K67/027, C12N5/10, C12Q1/68, G01N33/50, C12N15/00,
C12N5/00
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Score 7.8; DB 1; Length 11;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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THE MISTAR INSTITUTE
Nus musculus (mouse)
Nus musculus (mouse)
PD 05-FEB-2002
PP 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/014737, 26-AUG-1998 US 60/102051
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Key
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Sequence 9510 from Patent W002053774.
AX632468 1 GI:28468083
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/db_xref="taxon:9606"

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    /organism="Mus musculus"
/mol_type="genomic DNA"

    27.9%;
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Homo sapiens
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Best Local Similarity 81.8
Matches 9; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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81.8%; Pred. No. 1.5e+02;
ive 0; Mismatches 2; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 9300 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 8793 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                      Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Hether: WO 0205374-A 8487 11-UUI-2002; Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 9300 from Patent WO02053774.
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Sequence 8793 from Patent WO02053774.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX632258.1 GI:28467873
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AX631751.1 GI:28459858
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Best Local Similarity 81.8
Matches 9; Conservative
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AR027883/c
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Colote,S. and Pirotzky,E.
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/organism='Mus musculus (mouse)'.
Location/Qualifiers
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81.8%; Pred. No. 1.5e+02;
iive 0; Mismatches 2; Indels
                                             Score 7.8; DB 1; Length 11;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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THE WISTAR INSTITUTE
ON Mus musculus (mouse)
PD 2002503460-A/272
PD 05-FEB-2002
PP 12-FEB-1999 US 2000531545
PR 13-FEB-1999 US 60/102051
PR 13-FEB-1999 US 60/102051
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Compositions and method for healing wound.
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20 Squence 25 from Patent EP0692535.
A47665.1 GI:2301606

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JP 2002503460-A/272.
Mus musculus (house mouse)
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Best Local Similarity 81.8%;
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1 (bases 1 to 12)
Colote, S. and Pirotzky, E.
Oligonucleotides to inhibit the expression of isoprenyl protein transferases
Patent: US 5856461-A 25 05-JAN-1999;
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0; Mismatches 2; Indels
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Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 2;
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unidentified
unidentified
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1 (bases 1 to 12)
Pallisgaard,N. and Hokland,P.
Pallisgaard,N. and Hokland,P.
Pathisgaard,N. and Hokland,P.
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Other publication BR 9503015 960604
Other publication NZ 27239 960426
Other publication HU 71339 960326
Other publication JP 8051985 960227
Other publication FR 2721930 960105
Other publication FR 2721877 960105
Other publication PR 953170 951230
Other publication PL 309384 960108
Other publication NO 952601 960102
Other publication CA 2152233 951230
Other publication GA 2152233 951230

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Seguence 25 from patent US 5856461.
AR027883. GI:5938703

    .12
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Sequence 23 from Patent WO9824928.
A01496
A91496.1 GI:6740451
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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Page 67

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Gaps

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PAT 31-JAN-2002

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Logury of complifying DNA fragment, amplification apparatus of DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method and device for amplifying DNA fragment
Patent: JP 2000270867-A 25 03-0CT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FOREGRRY AND FISHERIES
OS Unidentified
PD 03-0CT-2000
PP 19-MAR-1999 JP 1999076844
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Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
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Method and device for amplifying DNA fragment.
E38651
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Location/Qualifiers
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C12N15/09,C12M1/00,C12Q1/68,C12N15/00
Strandedness: Single;
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Best Local Similarity 81.8%; Pred. No. 1.7e
Matches 9; Conservative 0; Mismatches
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Location/Qualifiers
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E64077
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TP 1999341989-A/25.
synthetic construct
synthetic construct
artificial sequences.
I (bases 1 to 12)
Koichi, I.
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JP 2000270867-A/25.
unidentified
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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unclassified.
1 (bases 1 to 12)
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E64077/c
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E38651/c
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Method for amplifying DNA fragment, method for estimating state of method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste maicroorganism existing and method for estimating state of waste patent: JP 199276176-A 25 12-COT-1999

PD 12-COT-1999

PP 31-MAR-1998 JP 1998087652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of microorganism existing and method for estimating state of waste. E29545.1 GI:13021048
JP 1999276176-A/25.
unidentified
unclassified.
l (bases 1 to 12)
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Method of amplifying DNA fragment, apparatus for amplifying DNA
fragment, method of assaying microorganisms, method of analyzing
microorganisms and method of assaying contaminant
microorganisms and method of assaying
patent: US 6287769-A 25 11-SEP-2001;
Location/Qualifiers
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PC C12N15/09,809B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
Strandedness: Single;
Location/Qualifiers
FT source 1. .12
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                                                                                  27.9%; Score 7.8; DB 1; Length 12;
81.8%; Pred. No. 1.76+02;
ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                          12 bp | Sequence 25 from patent US 6287769.
     Location/Qualifiers
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PAT 26-SEP-2002

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Bailly, J. E. and Durbin, A.P. Attenmated human-bovine chimeric parainfluenza virus (piv) vaccines Patent: WO 0104320-A 26 18-JAN-2001; THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US) Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown.
Unclassified.
11 (bases 1 to 12)
Dale, R.M.K.
Arrays with modified oligonucleotide and polynucleotide
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27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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           ErbB2/neu targeted ribozymes
Patent: US 5599704-A 107 04-FEB-1997;
Location/Qualifiers
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Compositions
Patent: US 6440723-A 9 27-AUG-2002;
Location/Qualifiers
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Sequence 26 from Patent WO0104320.
AX073604
AX073604.1 GI:12710027
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Sequence 9 from patent US 6440723.
AR224412
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synthetic construct
artificial sequences.
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Best Local Similarity
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AR224412
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Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substanting 
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Duyao,M.P., MacDonald,M.E. and Gusella,J.F.
Transport protein gene from the Huntington's disease region
Patent: US 5538844-A 19 23-UUL-1996;
Location/Qualifiers
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Location/Qualifiers
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81.8%; Pred. No. 1.7e+02;
rative 0; Mismatches 2; Indels
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
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Sequence 107 from patent US 5599704.
135021 13:021.1 GI:2087989
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Sequence 19 from patent US 5538844.
123754
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Unclassified.
1 (bases 1 to 12)
Thompson,J.D. and Draper,K.G.
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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Bailly,J.E. and Durbin,A.P.
Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines
Patent: Wed 010420-A 31 18-JAN-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
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/noTe="Sequence flanking Bsi W1 site in rBPIV3 of sFHINH"
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Patent: WO 0123620-A 9 05-APR-2001;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthesized oligonucleotide"
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Sequence 55 from Patent WO0202605.
                                                                                          Sequence 31 from Patent WO0104320.
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Sequence 9 from Patent W00123620.
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AX105625.1 GI:13921655
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Skiadopoulos,M.H., Collins,P.L., Murphy,B.R. and Schmidt,A.C. Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines Patent: WO 10202605-A 60 10-JAN-2002; THE SECRETARY, DEPARAMENT OF HEALTH AND HUMAN SERVICES (US) Location/Qualifiers
                                                                                                         Skiadopoulos,M.H., Collins,P.L., Murphy,B.R. and Schmidt,A.C.
Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines
Patent: WO 0202605-A 55 10-JAN-2002;
THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
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Parisgard, N. and Hokurando, P. Method for detecting abnormality in chromosome
Patent: JP 2001505428-A 23 24-APR-2001;
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Best Local Similarity 81.8%; Pred. No. 1.7e+02;
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Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Method for detecting abnormality in chromosome.
BD023278
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Sequence 60 from Patent W00202605.
AX454110
AX454110.1 GI:21713748
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JP 2001505428-A/23.
Homo sapiens (human)
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Shannon,M., Gu,Y. and Nguyen,C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 63.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 7; Indels
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Aeomica, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.7e+02;
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                          JP 2001505428-A/23
24-APR-2001
08-DEC-1997 JP 1998525090
NEILLS PARLSGARD, PATER HOKURANDO
C12N15/09,C12Q1/68,G01N33/50,C12N15/00
Strandedness: Single;
                                                                                                                                                                                              Topology: Linear;
/desc = 'DNA (synthetic)'
Key
Location/Qualifiers
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Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 2842 from Patent EP1281758.
AX690110.1 GI:29412968
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Sequence 2841 from Patent EP1281758.
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                1. .12
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/mol_type="genomic DNA"
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Homo sapiens
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NEILLS PARISGARD
PN JP 20155428
PD 24-APR-2001
PF 08-DEC-1997 (
PI NEILLS PARISC
C C12N15/09/C1/
CC Strandedness
CC Topology: Lin
CC Topology: Lin
FH Key
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Best Local Similarity
Matches 9; Conserv
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FERENCE AUTHORS TITLE

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MATURES

Matches

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Gaps

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PAT 31-MAR-2003

linear

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shannon,M., Gu,Y. and Nguyen,C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
                                                                                                                                                                                                                                                                                     Shannon,M., Gu,Y. and Nguyen,C.T. Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                    mdz12
Patent: EP 1281758-A 2843 05-FEB-2003;
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Acomica, Inc. (US)
Location/Qualifiers
                                                                                                                25 bp D1
Sequence 2843 from Patent EP1281758.
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Sequence 2844 from Patent EP1281758.
AX690112.1 GI:29412970
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Location/Qualifiers
4 GCCCTACGTGTACAGGGAG 22
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                              24 GCACTCGCTGCACACGTAG 6
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Homo sapiens
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AUTHORS
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VERSENON

AXO96928.1 GI:13513196

VERSENON

AXO96928.1 GI:13513196

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AXO96928.1 GI:13513196

VERSENON

AXO96928.1 GI:13513196

KEYWORDS

Homo sapiens

ENKARYOLA;

Homo sapiens

CACATAILA

Homo sapiens

CACATAILA

REPERENCE

Homo sapiens

CACATAILA

Nammalia; Entheria; Primates; Vertebrata; Enteleostomi;

Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.O. and

TITLE

AUTHORS

Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.O. and

TITLE

AUTHORS

Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.O. and

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AUTHORS

Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.O. and

TITLE

AUTHORS

Location Qualifiers

Location Qualifiers

Location Qualifiers

Location Conservative

Location Similarity

ADECTION

AND LYPS=""Lander Job" DB 1; Length 10; Matches"

ADECTION Match

T. Conservative

L. Mismatches

T. Secse

Job time: 2 secse
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

BP.

ABV68894 standard; cDNA; 11

11 ACAGGGAG 4

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(first entry)

21-OCT-2002

ABV68894;

Human skin EST 6680

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skin ageing and/or stress, and identifying or determining the effects of pharmaceutical or cosentical agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
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                                                                                                                                                                          Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
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Best Local S:
Matches 8
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ABV68516/C
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Conradt M, Hofmann K;

Petersohn D,

WPI; 2002-590638/63.

(HENK ) HENKEL KGAA.

20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127

WO200253774-A2

11-JUL-2002.

Homo sapiens.

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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; soleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; scasdea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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Best Local Similarity 100.
Matches 8; Conservative
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RESULT 53
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28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels

Local Similarity 100.

Best Loca Matches

Query Match

15 ACAGGGAG 22

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

Claim 24; Page 310; 1345pp; German.

e.g. skin cancer.

Petersohn D, Conradt M, Hofmann K;

(HENK ) HENKEL KGAA

WPI; 2002-590638/63.

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or disorders, specifically neurodermatitis; sunburn; specifically neurodermatitis; sunburn; specifically neurodermatitis; sunburn; specifically respect sections in the present sequence is that of a human expressed sequence tag skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
immunosuppressive; antinflammatory; octostaric; SAGS; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence rag; ss.
Human, skin, dermatological, vulnerary, antipsoriatic; antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis; psoriasis; dermatitis; skin cancer; EST, expressed sequence tag, ss.
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                                                                                                                                                                                                                                                                                              Petersohn D, Conradt M, Hofmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 24; Page 255; 1345pp; German.
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Best Local Similarity 100.
Matches 8; Conservative
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeocrasis, to determine skin homeocrasis and to test agent (A) that maintains or promotes skin homeocrasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; acopic dermatitis; acne; sebornhea; lupus erythematouus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosace; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention 88888888888888888888

Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

ö 28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels 8; Conservative Best Local Similarity Matches 8; Conserv Query Match

15 ACAGGGAG 22 ACAGGGAG 9 ď ò

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ABV67037 standard; cDNA; 11 BP RESULT 538

(first entry) 21-OCT-2002

ABV67037;

Human skin EST 4823

Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

Homo sapiens.

40200253774-A2.

11-JUL-2002

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127

(HENK ) HENKEL KGAA

Petersohn D, Conradt M, Hofmann K; 4PI; 2002-590638/63 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 158; 1345pp; German

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriatis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; soacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag ABV6703777

ABV6703777

ABV6703777

ABV6 ABV6

ABV6 ABV

Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other; g

ö DB 1; Length 11; 2.7e+02; Indels / Match 28.6%; Score 8; DB: Local Similarity 100.0%; Pred. No. 2.7 les 8; Conservative 0; Mismatches Query Match Matches

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Gaps

21 AGTCCAGG 28 ო 10 AGTCCAGG

RESULT 539

ABV70819 standard, cDNA; 11 BP.

ABV70819;

(first entry) 21-OCT-2002

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Human skin EST 8605.

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag; ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002.

20-DEC-2001; 2001WO-EP015179.

(HENK ) HENKEL KGAA.

03-JAN-2001; 2001DE-01000127.

Hofmann K; Petersohn D, Conradt M,

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Claim 24; Page 275; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically schooled from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriaals; scleroderma; inchthyosis, atopby dermatitis, acne, seborrhea; lupus erythematosus; rosaces; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag of the invention 

Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Gapa ö 28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 8, Conservative

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12 TGTACAGG 19

4 TGTACAGG 11

RESULT 540 ABV64705

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; ichthyosis; melanoma, basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Best Local Similarity 100.0
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                                                                                                                                                                             Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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    ABV64705 standard; cDNA; 11
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Gaps ..

Petersohn D, Conradt M, Hofmann K;

Homo sapiens

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WPI; 2002-590638/63
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure, Page 94; 1345pp; German

The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

0; Gaps 28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels Query Match 28.6 Best Local Similarity 100. Matches 8; Conservative

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ABV65110 standard; cDNA; 11 BP.

(first entry) 21-OCT-2002 ABV65110;

Human skin EST 2896

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

WO200253774-A2.

11-JUL-2002

03-JAN-2001; 2001DE-01000127.

20-DEC-2001; 2001WO-EP015179.

(HENK ) HENKEL KGAA

Hofmann Σ Petersohn D, Conradt

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 105; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to 

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determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis, atopic dermatitis, acne; seborrhea; lupus erythematosus; croscea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BST) of the invention
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Sequence 11 BP, 3 A, 2 C, 3 G; 3 T; 0 U; 0 Other;

ô Gaps ö DB 1; Length 11; ., 2.7e+02; ches 0; Indels 28.6%; Score 8; DB 1 100.0%; Pred. No. 2.7 :ive 0; Mismatches Query Match
Best Local Similarity 100.
Matches 8; Conservative

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RESULT 544 ABV71864/

ВР. ABV71864 standard; cDNA; 11

ABV71864;

21-OCT-2002 (first entry)

Human skin EST 9650

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002.

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127

(HENK ) HENKEL KGAA

Hofmann K; Petersohn D, Conradt M,

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer. 

Claim 24; Page 312; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (\$AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaais, scleroderma; ichthyosis, atopic dermatitis, acne; seborrhea; lupus erythematosus; sosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Gaps ö Indels Query Match 28.6%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 8; Conservative 0; Mismatches 0; Indels

Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

Human skin EST 1184

7 CTACGTGT 14

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11 CTACGTGT 4

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The invention relates to in vitro identification (WI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psorlaals; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (ESI) of the invention
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                                                                                                                                                                                                                                                                                                                                                                           Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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100.0%; Pred. No. 2.7
tive 0; Mismatches
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                                                                         ABV65919 standard; cDNA; 11 BP.
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Best Local Similarity luv.
8; Conservative
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                                                                                                                                                                                                                                                    ABV64393 standard; cDNA; 11 BP
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Best Local Similarity 100.
Matches 8; Conservative
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W0200253774-A2

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ABV63398 standard; cDNA; 11

546

GGGAGTCC 25 GGGAGTCC 11

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(first entry)

21-OCT-2002

ABV63398;

RESULT 54
ABV63398
ID ABV6
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AC ABV6
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DT 21-0

11-JUL-2002

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (\$AGS) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BST) of the invention

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

Disclosure; Page 57; 1345pp; German.

e.g. skin cancer.

Hofmann K;

Petersohn D, Conradt M,

WPI; 2002-590638/63

(HENK ) HENKEL KGAA.

20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127

WO200253774-A2

11-JUL-2002.

Homo sapiens

Mon Apr 19 15:55:12 2004

Page 243

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The invention relates to in vitro identification (M1) of genes expression in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. ($AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                   In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                                 Hofmann K;
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20-DEC-2001; 2001WO-EP015179.
                                          03-JAN-2001; 2001DE-01000127
                                                                                                                              Petersohn D, Conradt M,
                                                                                  (HENK ) HENKEL KGAA
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28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 8; Conservative 20 GAGICCAG 27 ઠ

11 GAGTCCAG 4 엄

ABV64443 standard; cDNA; 11 BP 21-OCT-2002 ABV64443; 548 

(first entry) Human skin EST 2229

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens.

40200253774-A2

11-JUL-2002

03-JAN-2001; 2001DE-01000127.

20-DEC-2001; 2001WO-EP015179.

(HENK ) HENKEL KGAA.

Petersohn D, Conradt M, Hofmann K;

NPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 87; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaals, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention 

Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Gaps ., 0; Indels DB 1; Length 11; . 2.7e+02; 28.6%; Score 8; DB 1 100.0%; Pred. No. 2.7 tive 0; Mismatches Query Match Best Local Similarity 100... Best Acad 8; Conservative

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ABV72049 standard; cDNA; 11 BP.

ABV72049;

(first entry) 21-OCT-2002

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Gaps . Human skin EST 9835

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002.

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127

(HENK ) HENKEL KGAA.

Hofmann K; Petersohn D, Conradt M,

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Claim 24; Page 319; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the 

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RESULT 550 **ABV69736** 

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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE$) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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immunosuppressive, antiinflammatory, cytostatic, SAGE; neurodermatitis;
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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                                                               ABV66268 standard; cDNA; 11 BP.
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                                                                                                         28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0; Indels
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                                                                                                                 Query Match 28.6
Best Local Similarity 100.
Matches 8; Conservative
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Gaps ö

Best Loca Matches

Hofmann K;

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The invention relates to in vitro identification (WI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(MI) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                                                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 213; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-2001; 2001WO-US024031
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                                                                                                                                 20-DEC-2001; 2001WO-EP015179.
                                                                                                                                                                 03-JAN-2001; 2001DE-01000127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL91942 standard; cDNA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2002 (first entry)
                                                                                                                                                                                                                                  Petersohn D, Conradt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 8; Conservative
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                                                                                                                                                                                                                                                                4PI; 2002-590638/63
                                                                                                                                                                                                (HENK ) HENKEL KGAA
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                                                               WO200253774-A2
                                 Homo sapiens.
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                                                                                                 11-JUL-2002
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useful for
in the 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
                                                                                                                                                                                                                                     An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel primer pairs and sequence determination oligonucleotides amplifying and detecting novel single nucleotide polymorphisms flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.78+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                  Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 325; 331pp; English.
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                                                                              (UYJO ) UNIV JOHNS HOPKINS
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                  Kinzler KW,
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                                                                                                                                                                                       WPI; 2002-291856/33.
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                                                                                                                                  St Croix B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK68760;
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0; Gaps

28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels

of the human CYP3A4 gene

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Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
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SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to PCR primer pairs for amplifying and sequence determination oligonucleorides for detecting single nucleoride polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450 (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position 6fl of a defined 1345 base pair sequence for CYP3A4 or position 957, 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9. The PCR primers are useful for amplifying the CYP sequences and the oligonucleotides are useful for detecting SNPs in the 5'-flanking regions of the CYP3A4 or CYP2C9 genes. ABK68755-ABK68761 represent
                                               The present invention relates to PCR primer pairs for amplifying and sequence determination oligonucleotides for detecting single nucleotide polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450 (CVP) genes encoding CYP3A4 or CYP2C3. The SNPs correspond to position 461 of a defined 1345 base pair sequence for CYP3A4 or position 557, 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2A9. The PCR primers are useful for amplifying the CYP sequences and the oligonucleotides are useful for detecting SNPs in the 5'-flanking regions of the CYP3A4 genes. ABK68755-ABK68761 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel primer pairs and sequence determination oligonucleotides useful for amplifying and detecting novel single nucleotide polymorphisms in the 5' flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide #5 for detecting SNP in 5'-region of human CYP3A4 gene.
                                                                                                                                                                                                                                  28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Risinger C, Andersson MK, Lewander T, Olaisson E;
                                                                                                                                                                                                           Sequence 11 BP; 3 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 17; 47pp; English.
                          Claim 4; Page 17; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                   ABK68759 standard; DNA; 11 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                       11 GTGTACAG 18
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                                                                                                                                                                                                                                                                                                                                                                                                            ABK68759;
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                        RESULT 555
                                                                                                                                                                                                                                                               Matches
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The present invention describes a method for detecting a polymorphism (P) in polymucleotide with fragments of (N) segments which contain a clippoutleotides with fragments of (N) segments which contain a polymorphism, and have modified nucleotides that are incorporated at each polymorphism, and have modified nucleotides that are incorporated at each point of occurrence of suspected (P) during amplification; and (2) analypsing the hybridising fragments for an incorporated detectable label identifying the susceptible polymorphism. The method is used for detecting polymorphisms (e.g. a single nucleotide polymorphism (SNP), a checting polymorphism (N). The method is useful for developing diagnostic and prognostic tools for detecting a predisposition of certain disease and disorders. The method is useful for detecting variance in DNA sequencing, and has applications in genotyping. The present sequence represents a transferrin receptor gene related oligonucleotide sequence, which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting polymorphism in a polymucleotide (N) comprises hybridizing oligomucleotide with a variant (N) having modified nucleotides incorporated at each point of suspected polymorphism occurrence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferrin receptor gene related oligonucleotide fragment #7.
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                       28.6%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.7e+02; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                       ABL51577 standard; DNA; 11 BP
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Query Match
Best Local Similarity 100.
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Matches 8; Conservative
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                                                                                                                                                   11 GTGTACAG 18
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                                                                                                                                                                                                                3 GTGTACAG 10
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                                                                                                                                                                                                                                                                                                          RESULT 556
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557

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histocompatibility complex (WHC), esp. for typing denors for bone marrow transplants, involves determining if the denor tissue HLA-DR alleles are selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNewl, DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and DR1a-c. The method uses PCR to amplify these regions followed by sequence-specific oligomucleotide probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH allows detection of polymorphisms that predict differences at a single amino acid level thus reducing errors and improving the chance of successfully matching tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel method of typing the human leukocyte antigen (HLA) of the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human leukocyte antigen; HLA, allele; HLA-DR*08; HLA-DR*12; locus Bl; polymorphism; amplify; conserved region; detection; primer; probe; tissue matching; identifying disease susceptibility; ss.
                                                                                  Tissue typing, human leukocyte antigen, HLA; MHC; donor, allele; PCR; major histocompatibility complex; bone marrow transplant; primer; amplification; polymerase chain reaction; probe; polymorphism; sequence-specific oligonucleotide probe hybridisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Improved method for HLA typing - by DNA amplification and sequence-specific oligo:nucleotide hybridisation, used to select bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                     (BLOO-) BLOOD CENT RES FOUND INC.
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(first entry)
(first entry)
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                                          HLA-DR typing probe L74.
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                                                                                                                                                                                                                                                                                                                                08-APR-1993;
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  17-AUG-1999
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18-DEC-1996
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                                                                                                                                                                                                 Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal polynuclectic equences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiodendial cells in a patient, or for identifying candidate drugs for treating tumours. ABX71828-ABX71899 represent DNA tags for human PEM, TEM or NEM genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                 Tumour endothelial marker; normal endothelial marker; PEM;
pan-endothelial marker; polycystic kidney disease; psoriasis;
diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
necangiogenesis; immune response; cytostatic; antidiabetic;
ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
                                                                                                                                                                                                                                                              endothelial cell; EC; tumour endothelial cell; TEM; NEM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinzler KW, Vogelstein B;
                                                                                                                                                                                                                      DNA tag used to identify human gene encoding PEM 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 93; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX79373 standard; DNA; 12 BP.
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                                                                                    ABX71867 standard; DNA; 11 BP
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                                                                                                                                                                         (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200283874-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                         12-MAR-2003
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Gaps

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Indels

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13-AUG-1996.

AAX79373

AAX79373 ID AAX7 XX AC AAX7

RESULT 558

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Best Loc Matches

WPI; 1996-383664/38.

Baxter-Lowe LA;

27-JUN-1990;

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Probes AAV16561-624 are used to identify differences in the DR region of human major histocompatibility complex (HLA-DR). The specification describes a method for HLA-typing, which includes an oligonucleotide probe which undergoes sequence-specific hybridisation with an HLA-DR beta consensus sequence at positions 61-64. The probe contains a labelling substance other than a nucleotide sequence, which facilitates detection of the probe. The HLA sequence of subject is PCR amplified, and a probe that recognises an allelic polymorphism at a selected HLA locus is contacted with the amplified product. This first probe recognises a HLA-DR beta of the amplified product. This first probe recognises a HLA-CONTACT with a second sample of the amplified DNA in a separate reaction, and hybridisation detected. The probes and primers are used for HLA-typing, e.g. for tissue, especially bone marrow, transplants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 293614 for detecting SNP TSC0015707.
                                                                                                                                                                                                                                                                                                                                                                                                      Oligo:nucleotide probes and primers and methods for HLA typing particularly for tissue typing for bone marrow transplants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.6%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 19; 20pp; English
                                                                                                                                                                                                                                        (BLOO-) BLOOD CENT RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABH93621 standard; DNA; 12 BP.
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                                                                                                                                93US-00057957
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Matches 8; Conservative
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                                                                          30-DEC-1997.
                    US5702885-A.
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                                                                                                                                                                                                                                                                                             Human leukocyte antigen typing of tissue samples - using allele-specific amplification to distinguish allele pairs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR region, major histocompatibility complex; HLA-DR; HLA-typing;
HLA-DR beta consensus sequence; allelic polymorphism;
HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.
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28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                BLOO-) BLOOD CENT RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                              Example 1; Col 19; 24pp; English
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                    01-MAR-1993; 93US-0002503B.
                                                                       90US-00544218
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12-JUN-1998 (first entry)

AAV16569;

RESULT 560

Homo sapiens

Synthetic

1 CGGGCCCT 8

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WPI; 2001-657177/75

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but the blub/published\_pot\_sequences Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 293614; 29pp + Sequence Listing; German.

Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match

28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 8 TACGIGIA 15 |||||||| 12 TACGTGTA 5

0; Gaps

0; Indels

ABI06748 standard; DNA; 12 (first entry) 22-FEB-2002 ABI06748; 

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 306721 for detecting SNP TSC0022148.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Olek A, Piepenbrock C,

WPI; 2001-657177/75

... T Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 306721; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

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Gaps

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Query Match 28.6%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 3.18+02; Matches 8; Conservative 0; Mismatches 0; Indels

Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH0010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF99989, ABF0010-ABF99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at figures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 8; Conservative
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ABH95544
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                                                                                                                                                                                                     SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 356331 for detecting SNP TSC0050060.
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nes 8; Conservative 0
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            CCCTACGT 12
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ABH70251
ID ABH702
XX
AC ABH702
XX
DT 22-FEB
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Matches
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ABH70251 standard; DNA; 12 BP.

22-FEB-2002 (first entry)

ABH70251;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at the printed specification, but fire wipo int/pub/published_pct_sequences
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                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 270228 for detecting SNP TSC0002052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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Best Local Similarity
Matches 8; Conserv
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity luv.
18 Conservative
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ABH92486/c
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                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
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06-APR-2001; 2001WO-IB000713.
                                                    07-APR-2000; 2000DE-01019173
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                                                                                                         (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                              methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Claim 1; SEQ ID NO 292479; 29pp + Sequence Listing; German.

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Sequence 12 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
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                                      Query Match
Best Local Similarity 100.'
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AB111
AB11
AB111
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Gaps

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0; Indels

Berlin K;

Claim 1; SEQ ID NO 313383; 29pp + Sequence Listing; German.

0; Indels

Query Match 28.6%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels

5 CCCTACGT 12 |||||||| 5 CCCTACGT 12

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ABI62488 standard; DNA; 12 BP.

22-FEB-2002 (first entry)

ABI62488;

Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other; was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                                                                                                                                                                                                                                                                            SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 313957 for detecting SNP TSC0026047.
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28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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AD 113984
AD 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; Oligonucleotide primer SEQ ID NO 295535 for detecting SNP TSC0016627.

ABH95542 standard; DNA; 12 BP.

22-FEB-2002 (first entry)

0; Gaps 0;

Ouery Match
28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels

TACGIGIA 15 racerera 11

8 8

Sequence 12 BP; 4 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Gaps

Claim 1; SEQ ID NO 362461; 29pp + Sequence Listing; German.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG.

RESULT 569
AB162488
AC AB16248
AC AB1626
AC AB

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2. Homo sapiens.

18-OCT-2001.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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 central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 100.v.
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                              Homo sapiens.
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ABH76707
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 376075 for detecting SNP ISC0061603.
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                                                                                                                                                 Claim 1; SEQ ID NO 276700; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          28.6%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 3.18+02; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
....hes 8; Conservative
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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Piepenbrock C,

olek A,

WPI; 2001-657177/75

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF0010-ABF9989 and ABI00010-ABI32073 typesent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligomicaleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, caligometrs are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI0010-ABF82073 represent the oligometrs described in the invention. NoTE: The sequence data for this partent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 281698 for detecting SNP TSC0010001.
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                                                                                                                                                                                                                                                                 28.6%; Score 8; DB 1; Length 12;
llarity 100.0%; Pred. No. 3.1e+02;
Conservative 0; Mismatches 0; Indels
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ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 285822 for detecting SNP TSC0012462.
                                             Gabs
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100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
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ABH86354
ID ABH86354 standard; DNA; 12 BP.
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ABH85829 standard; DNA; 12
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Best Local Similarity 100.
Matches 8; Conservative
Query Match
Best Local Similarity 100.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                            Oligonucleotide primer SEQ ID NO 286347 for detecting SNP TSC0012678.
                                                                                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 286347; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was obtained in electronic format from WI
ftp.wipo.int/pub/published_pct_sequences
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                      (first entry)
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                                                                                                                Homo sapiens.
                      22-FEB-2002
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ABH86354;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH0010-ABH99989 and ABI00010-ABI82073 the present the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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17 AGGGAGTC 24 AGGGAGTC 12

ABI13988 standard; DNA; 12 22-FEB-2002 ABI13988; RESULT 577 ABI13988
ILD ABI13
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ILD ABI13988
ILD ABI1398
ILD A

Oligonucleotide primer SEQ ID NO 313961 for detecting SNP TSC0026047. (first entry)

ВЪ.

SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH0010-ABF99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at Gaps Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. ö Claim 1; SEQ ID NO 313961; 29pp + Sequence Listing; German Query Match 28.6%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels Sequence 12 BP; 3 A; 2 C; 3 G; 4 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequences Berlin K; 06-APR-2001; 2001WO-IB000713 07-AFR-2000; 2000DE-01019173 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG 8 TACGTGTA 15 WPI; 2001-657177/75 18-OCT-2001. ઠે

Oligonucleotide primer SEQ ID NO 297053 for detecting SNP TSC0017414. ABH97060 standard; DNA; 12 BP. (first entry) 2 TACGIGTA 9 22-FEB-2002 ABH97060; RESULT 578 ABH97060/ g

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. WO200177384-A2 Homo sapiens. 18-OCT-2001. 

Berlin K; 07-APR-2000; 2000DE-01019173 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75

06-APR-2001; 2001WO-1B000713.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                Claim 1; SEQ ID NO 297053; 29pp + Sequence Listing; German.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 356333 for detecting SNP TSC0050060.
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                                                                                                                                                          28.6%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 3.1e+02; Live 0; Mismatches 0; Indels
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                                                                                                                        Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
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Matches 8; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 310676 for detecting SNP TSC0024049.
                                                                                                                                          Oligonucleotide primer SEQ ID NO 328918 for detecting SNP TSC0034654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 328918; 29pp + Sequence Listing; German.
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Pred. No. 3.1e+02;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 8; Conservative 0
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                                ABI28945 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       designed to detect methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABC0010-ABE99889, ABC0010-ABE99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typuploublished_pot_sequences
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            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 100.00
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07-APR-2000; 2000DE-01019173

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                    Claim 1; SEQ ID NO 375376; 29pp + Sequence Listing; German.
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28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                (EPIG-) EPIGENOMICS AG
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                                                                                                  WPI; 2001-657177/75
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99899 and ABI00010-ABF80031 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published\_pct\_sequences This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but ftp.wipo.int/pub/published\_pot\_sequences SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 273565 for detecting SNP TSC0003234. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. ; Claim 1; SEQ ID NO 273565; 29pp + Sequence Listing; German DB 1; Length 12; 0; Indels Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other; 28.6%; Score 8; DB 1 100.0%; Pred. No. 3.1 iive 0; Mismatches Olek A, Piepenbrock C, Berlin K; ABH73580 standard; DNA; 12 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 (first entry) Similarity 100. 8; Conservative (EPIG-) EPIGENOMICS AG. 8 TACGIGIA 15 3 TACGTGTA 10 WPI; 2001-657177/75. WO200177384-A2 Homo sapiens. 22-FEB-2002 18-OCT-2001. Query Match Best Local S: Matches ABH73580; ABH73580 ò 음 0; Gaps

typing, i cytosine

Claim 1; SEQ ID NO 363232; 29pp + Sequence Listing; German.

Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and

methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 359372 for detecting SNP TSC0051583.
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tive 0; Mismatches
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                                      ABI59399 standard; DNA; 12 BP.
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Matches 8, Conservative
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                                                                                                    ABI59399;
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AAF92629
ABI 59 39 9/6
XXX ABI 15, ABI 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonuclectide primers or peptide nucleic. acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 356623 for detecting SNP TSC0050224.
                                                                                                                                                                   Gaps
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                                                                                                                                                            0; Indels
                                                                                          Similarity 100.0%; Pred. No. 3.1e+02; 8; Conservative 0; Mismatches 0; Indels
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                                  Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
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Matches 8; Conservative
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                                                              Sequence 12
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                                                                                                                                                     RESULT 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen typing by amplifying a sample followed by sequence specific oligonucleotide hybridization with labeled oligonucleotide probes that hybridize with a series of known control DNA
                                                                                                                                                                                 The present invention relates to human leukocyte antigen (HLA) typing. The method involves detecting polymorphic residues by sequence specific oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
                                                                                                                           Human leukocyte antigen typing by amplifying a sample followed by sequence specific oligonucleotide hybridization with labeled oligonucleotide probes that hybridize with a series of known control DNA
                                                                                                                                                                                                                                                                                                                                                                                                Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
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                                                                                                                                                                   Disclosure; Col 11-14; 16pp; English.
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                                                                             (BLOO-) BLOOD CENT RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                AAF92695 standard; DNA; 12 BP.
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                                      97US-00000805
                                                     90US-00544218.
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                                                                                             Baxter-Lowe LA, Gorski JA;
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Best Local Similarity 100.0%
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08-APR-1993;
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        US6194147-B1
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                       27-FEB-2001
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The invention relates to a polymerase chain reaction (PCR) based method of DNA fingerprinting, comprising using primers that match the conserved regions of a gene family. The method is useful for gene expression analysis of any cell or tissue, or for the performance of DNA fingerprinting analysis of the same organism in order that one will reveal the function of a gene that produced differential product between genotypes. The method is also useful for identifying PCR reactions that contain a gene of interest in a gene family reverse transcriptase (RT). PCR expression analysis. The method is also useful for identifying genes that belong to a gene family that might be involved in cancer formation. The method is particularly useful for comparing genomic sequences. These are also applicable in agriculture (e.g. to mark useful genes to assist breeding). The current sequence represents a plant cis-regulatory confiners that match the sequence of ubiquitous cis-acting regulatory
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                                                                The present invention relates to human leukocyte antigen (HLA) typing. The method involves detecting polymorphic residues by sequence specific oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fingerprinting; cancer; agriculture; breeding; PCR; primer; gene family; ds.
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(AGRI-) AGRIC RES ORG NEWE YA'AR RES CENTE.
Disclosure, Col 11-14; 16pp; English.
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02-JUL-2000; 2000IL-00137124.
20-AUG-2000; 2000IL-00137959.
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The invention relates to determining whether a subject has or is at risk of developing glaucoma, retinal degenerative disease, or a cardiovascular disease, comprises generating a transcriptional or translational profile (i.e. 'fingerprint') in the subject or in a sample obtained from the subject, based on the expression of the different myocilin (MYOC, also known as trabecular meshwork inducible glucocorticoid responsive protein, TIGR) mRNA species or polypeptide forms, where a difference in the profile relative to that in a normal subject indicates that the subject has or is at risk of developing the above-mentioned diseases. Also included are: (1) a method for establishing MYOC genetic population profile in a population of individuals having glaucoma, retinal degenerative disease, or a cardiovascular disease, or a cardiovascular disease, comprising determining MYOC genetic profile of an individual and comparing the individual's MYOC genetic profile to an individual and comparing the individual's MYOC genetic profile to an individual and a kit for determining whether a subject has or is likely
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                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; TIGR; MYOC; Myocilin; Glaucoma; blindness; trabecular meshwork inducible glucocorticoid responsive protein; retinal degenerative disease; RDD; retinitis pigmentosa; macular degeneration; Usher syndrome; dardiovascular disease; congenital heart disease; myocardial ischaemia; stroke; acute endocarditis; hypertensive heart disease; arrhythmia; arteriosclerotic heart disease.
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                                                                     DB 1; Length 12;
. 3.1e+02;
ches 0; Indels
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                                     Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
                                                                     28.6%; Score 8; DB 1
100.0%; Pred. No. 3.1
:ive 0; Mismatches
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                                                                                       Local Similarity 100.
Les 8; Conservative
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to develop glaucoma, retinal degenerative disease, or a cardiovascular disease, comprising a probe or primer which hybridises to the MYOC muchaic acid, or an antibody or peptide probe capable of specifically binding to the novel MYOC polypeptide(s), and instructions for use. The method is useful for the proposis and/or diagnosis of glaucoma, retinal degenerative diseases (RDD) or cardiovascular diseases (e.g. blindness, retinitis pigmentosa, macular degeneration, Usher syndrome, congenital heart disease, myocardial ischemia, stroke, acute endocarditis, hypertensive heart disease, arrhythmia and arteriosolerotic heart disease), and in screening assays for the identification of therapeutics and the evaluation of their effectiveness for treating the abovementioned diseases in a subject. The present sequence represents the 3' flanking sequence surrounding the deletion present in a MYOC cDNA variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism, biallelic; human, forensic; paternity testing, disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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Pred. No.
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100.0%; Pre
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Gaps ; 0

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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis; atophy dermatitis, anner, seborrhea; lupus expressedsus inchangual cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                            DB 1; Length 15;
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                                                                                                                                                                       Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
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Pred. No. 4e+02;
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100.0%; Pred. No. ...
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                                                                                                                                    prophylaxis of such diseases
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Best Local Similarity 100.
Matches 8; Conservative
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ABV65206
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1; Length 11;

27.9%; Score 7.8; DB 1 81.8%; Pred. No. 3e+02;

Query Match Best Local Similarity

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The present invention relates to a new CYP3A5 polymucleotide encoding a polymeptide, where the polymucleotide is capable of hybridising to a (CYP3A5 gene. The invention is useful in an in vitro method for identifying a polymorphism. The invention is also useful for useful for diagnosing a disorder related to the presence of a molecular variant of CYP3A5 or susceptibility to such a disorder, where the disorder is cancer, or diseases including cardiovascular diseases, diabetes and AIDS. The invention can further be used for the preparation of a diagnostic composition for diagnosing a disease in a subject having a genome comprising a variant allele of the cYP3A5 gene, where the subject is an African American. The molecules of the invention are as forensic markers and in pharmacological studies. The present nucleic acid sequence represents a human CYP3A5 gene polymorphism reference DNA sequence, as described in the invention
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                                                                                                                                                                                                                                                                             Human, CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes; AIDS; African American; forensic marker; pharmacological; cytostatic; antidiabetic; anti-HIV; gene therapy; ds.
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   Mismatches
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29-DEC-2000; 2000US-0258952P.
16-JAN-2001; 2001EP-00100172.
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16-AUG-2001; 2001EP-00118884.
16-AUG-2001; 2001US-0312825P.
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Query Match

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                                 7 CTACGTGTACA 17
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ABI23374;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at this pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                  central nervous system; gastrointestinal; respiratory; immune; metabolic.
peptide nucleic acid; cytosine methylation; cardiovascular; primer, ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      claim 1; SEQ ID NO 318372; 29pp + Sequence Listing; German.
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ABF18031 standard; DNA; 13
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Best Local Similarity 81.0
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                                                                                                                                                                                                                                                                                     peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 323347 for detecting SNP TSC0031342.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                    ABI23374 standard; DNA; 12 BP
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Matches 9, Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrohitestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF0010-ABF99999 and ABI00010-ABF9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitp.wipo.int/pub/published_pct_sequences
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ABF19283/
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                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 81.8%; Score 7.8; DB 1; Length 13; Similarity 81.8%; Pred. No. 3.8e+02; 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 118028; 29pp + Sequence Listing; German
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Oligonucleotide SEQ ID NO 119279 for detecting SNP TSC0029787.
                                    21-FEB-2002 (first entry)
            ABF19282;
This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                    Gaps
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                                                                                                                                                                                                                               Oligonucleotide SEQ ID NO 144692 for detecting SNP TSC0036396.
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         Score 7.8; DB 1; Length 13;
Pred. No. 3.8e+02;
1; Mismatches 3; Indels
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           27.9%;
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Best Local Similarity 69.2
Matches 9; Conservative
                                                           12 TGTACAGGGAGTC 24
      Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                           |||| | | |||:
13 TGTAAACGTAGTY 1
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 119279; 29pp + Sequence Listing; German.
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RESULT 601 ABF19282 ID ABF19282 standard; DNA; 13

12 TGTACAGGGAGIC 24

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06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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ID ABF36730 standard; DNA; 13
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Matches 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from MIPO at
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              diagnosis and cell typing, is
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                          designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                        Claim 1; SEQ ID NO 136727; 29pp + Sequence Listing; German.
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                oligonucleotides, useful for
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Best Local Similarity 81.6.
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Score 7.8; DB 1; Length 25; Pred. No. 5.3e+02; 0; Mismatches 7; Indels

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Query Match 27.9 Best Local Similarity 63.2 Matches 12; Conservative

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GCACTCGCTGCACGTAG

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ADB01856 standard; DNA; 25

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Gaps ö

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ12. MDZ3 is encoded at chromosome 742-1. MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 16p1.2 and MDZ12 is encoded at chromosome of chromosome 16p2.3-22.2, MDZ7 is encoded at chromosome 15q26.1. The MDZ3, MDZ4, MDZ1, and MDZ12 sequences are useful in therapy, of MDZ3, MDZ4, MDZ7, or MDZ12, encoder content of mDZ12. The nucleic acused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
oligomers are also used for detecting cell type differentiation. ABC00010-ABC39989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. Wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MDZ4; MDZ1; MDZ1; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23,
                                                                                                                                                                                      27.9%; Score 7.8; DB 1; Length 13; 81.8%; Pred. No. 3.8e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MDZ3 scanning oligonucleotide SEQ ID 2841.
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associated with decreased or incre
MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                             ADB01855 standard; DNA; 25 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gu Y, Nguyen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                    Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                              7 CTACGTGTACA 17
                                                                                                                                                                                                                                                                                                                     3 crccerriaca 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB01855;
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 605
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Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ1; MDZ4; MDZ1; MDZ12; chromosome 7g22.1; chromosome 6p21.3-2-2; chromosome 16p11.2; chromosome 15g26.1; cancer; developmental disorder; ss.

30-JUL-2002; 2002EP-00016874

EP1281758-A2 Homo sapiens

05-FEB-2003,

02-AUG-2001; 2001US-00922181

(AEOM-) AEOMICA INC

Shannon M, Gu Y, Nguyen C;

WPI; 2003-423107/40

Human MDZ3 scanning oligonucleotide SEQ ID 2842.

(first entry)

20-NOV-2003

ADB01856;

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proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 16p1.3-22.2, MD27 is encoded at chromosome 16p1.2 sequences are useful in therapy. Or in manufacturing a medicament for treating or preventing a disorder associated with decreased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27 or MD212, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel human zinc finger-containing
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Pred. No. 5.3e+02;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 63.2
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.

30-JUL-2002; 2002EP-00016874. 02-AUG-2001; 2001US-00922181

Homo sapiens EP1281758-A2 05-FEB-2003. Shannon M, Gu Y, Nguyen C;

(AEOM-) AEOMICA INC

WPI; 2003-423107/40.

Human MDZ3 scanning oligonucleotide SEQ ID 2839.

20-NOV-2003 (first entry)

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                                                                                                                                                     Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7g22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15g26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.9%; Score 7.8; DB 1; Length 25; 63.2%; Pred. No. 5.3e+02; tive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                             Human MDZ3 scanning oligonucleotide SEQ ID 2840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GCCCTACGTGTACAGGGAG 22
                                              ADB01854 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                    30-JUL-2002; 2002EP-00016874
                                                                                                                                                                                                                                                                                                                              02-AUG-2001; 2001US-00922181.
                                                                                                                                                                                                                                                                                                                                                                                 Shannon M, Gu Y, Nguyen C;
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Best Local Similarity 63.43,
Conservative
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                       (AEOM-) AEOMICA INC.
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                                                                                                                                                                                                                      Homo sapiens
                                                                                                   20-NOV-2003
                                                                                                                                                                                                                                                                         05-FEB-2003.
                                                                        ADB01854;
                      RESULT 607
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New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27 or MD212, e.g. cancer.

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12. MDZ3 is conceins and their coding sequences: MDZ3, MDZ4, MDZ12. MDZ12. MDZ3 is conceded at chromosome 7622.1, MDZ4 is encoded at chromosome 6521.3-22.2, MDZ7 is encoded at chromosome 16511.2 and MDZ12 or treating or preventing a disorder as sociated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12, rhe nucleic acused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ1; Chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 15q26.1; cancer; developmental disorder; ss.
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0
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Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 4 A; 7 C; 10 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MDZ3 scanning oligonucleotide SEQ ID 2843.
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Example 8; SEQ ID NO 2839; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GCCCTACGTGTACAGGGAG 22
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Local Similarity 63.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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24 GCACTCGCTGCACACGTAG 6

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ADB01853 standard; DNA; 25 BP.

608

RESULT 60 ADB01853/

ADB01853;

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ3 MDZ3, MDZ12, MDZ12. MDZ3 is encoded at chromosome 7422.1, MDZ4 is encoded at chromosome 6921.3-22.2, MDZ7 is encoded at chromosome 6921.3-22.2, MDZ7 is encoded at chromosome 6921.3-22.2, MDZ7 is encoded at chromosome 1691.2 and MDZ12 is encoded at chromosome 620 in manufacturing a medicament for treating or preventing a disorder or in manufacturing a medicament for treating or preventing a disorder or associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease acids and proteins are also useful for diagnosing or monitoring a disease acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The probes are protein in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger proctein; MD23; MD24; MD27; MD21; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                           New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.9%; Score 7.8; DB 1; Length 25; 63.2%; Pred. No. 5.3e+02; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                     MDZ4, MDZ7 or MDZ12, e.g. cancer
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                                                                                                                                                                       02-AUG-2001; 2001US-00922181
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nes 12; Conservative
                                                                                                                                                                                                            (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                                       WPI; 2003-423107/40.
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                  Homo sapiens
                                                      EP1281758-A2
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                                                                                           05-FEB-2003
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Matches
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Gaps ô

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is cenceded at chromosome 7422.1, MD24 is encoded at chromosome 6721.3-22.2, MD27 is encoded at chromosome 6521.3-22.2, MD27 is encoded at chromosome 16011.2 and MD212 is encoded at chromosome 16011.2 and MD212 is encoded at chromosome 16021.2 and MD212 is encoded at chromosome 16021.2 and MD212 sequences are useful in therapy, or imanifacturing a medicament for treating or preventing a disorder sessociated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are protein are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant; virucide, ophthalmological, keloid, skin discorder, Insulin-Ilke Growth Factor. I receptor; IGF-1; pityriasis; IGF binding protein, IGFBP-2; IGFBP3; inflammation, psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scaleroderma; vart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease;
                                                                                                                                                                               New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, NDZ7 or MDZ12, e.g. cancer.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 25 BP; 5 A; 6 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                       Example 8; SEQ ID NO 2844; 103pp; English.
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                 02-AUG-2001; 2001US-00922181
                                                                                                 Nguyen C;
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Best Local Similarity
                                                                                                                                           WPI; 2003-423107/40.
                                                         (AEOM-) AEOMICA INC
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(MURD-) MURDOCH CHILDRENS RES INST.

21-JUN-1999; 99US-0140345P. 21-JUN-2000; 2000WO-AU000693

WO200078341-A1

28-DEC-2000.

Page 270

Edmondson SR

Werther GA,

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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.
                                                                             Example 7; Page 53; 201pp; English.
        Wraight CJ,
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [GGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP3, which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which as useful for ameliorating the effects of psoriasis, F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, plaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, chain or skin, growth factor—mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Score 7.6; DB 1; Length 15; Pred. No. 4.8e+02; 0; Mismatches 4; Indels ch 1 Similarity 71.4%; 10; Conservative 0 5 CCCTACGTGTACAG 18 Query Match Best Local Similarity Best Loc Matches

Sequence 15 BP; 3 A; 8 C; 2 G; 2 T; 0 U; 0 Other;

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Gaps .. 0

> cacrececinació 15 612 ò 엄

AAF47955 standard; DNA; 15 BP IGFBP3 oligonucleotide #1375. (first entry) 30-MAR-2001 AAF47955; AAF47955 

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityliasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; kearlosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neoblation of the retina; ss.

WO200078341-A1 Homo sapiens

28-DEC-2000

21-JUN-2000; 2000WO-AU000693 21-JUN-1999; 99US-0140345P (MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; Werther GA, Wraight CJ,

WPI; 2001-041421/05

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The present invention relates to a method for ameliorating the effects of antisence coloraders. The method comprises contacting the skin with an antisense oligomucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomucleotide which can be used to design the antisense oligomucleotides of the present invention (see AAF45151 and AAF45153-745161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                      Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
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0
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                                                                                                                                            Example 7; Page 53; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTACGTGTACAG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
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                                                                                              inflammation.
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IGFBP3 oligonucleotide #1376. AAF47956 standard; DNA; 15 30-MAR-2001 (first entry) AAF47956; RESULT 613 AAF47956

Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid; skin disorder, Insulin-like Growth, receptor, IGF-1; pityriasis, IGF binding protein, IGFBP-3; Inflammation, psoriasis, pilaris, growth factor mediated cell proliferation, ichthyosis; serborrhoea; ruba, keratosis, nessis, necloderma, wart, skin cancer; sclerotic disease, hyperneovascular condition, hyperplasis, kidney disease; neovascular condition of the retina; ss. 

Homo sapiens.

WO200078341-A1

21-JUN-2000; 2000WO-AU000693

99US-0140345P 21-JUN-1999;

Wraight CJ, Werther GA, Edmondson SR; (MURD-) MURDOCH CHILDRENS RES INST.

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

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Example 7; Page 53; 201pp; English
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skin disorders. The method comprises contacting the skin with an antisense cligonuclectide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation.

Inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense AAP45153 or Oligonuclectides of the present invention (see AAF45151 and AAP45153 or F45161). The method is useful for ampliorating the effects of psoriasis, inthrusis, thus, plants, scaborthoea, keloids, keratosis, neoplasis, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperplasia
The present invention relates to a method for ameliorating the effects of
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Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

Gapa ô 27.1%; Score 7.6; DB 1; Length 15; 71.4%; Pred. No. 4.8e+02; tive 0; Mismatches 4; Indels Local Similarity 71.4%; les 10; Conservative Query Match Best Loca Matches

RESULT 614

ABA80105 standard; DNA; 17 BP ABA801 

24-JAN-2002 (first entry)

ABA80105;

HBA2 mutation correcting oligonucleotide SEQ ID NO: 2951.

Human; gene therapy, adenosine deaminase deficiency; p53; beta-globin, retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma, APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hyperchlesterolaemia; VGT1; syndrome; APP; PSEN1; antisense; UDP-qjucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss

Homo sapiens.

WO200173002-A2.

04-OCT-2001

27-MAR-2001; 2001WO-US009761.

27-MAR-2000; 2000US-0192176P. 27-MAR-2000; 2000US-0192179P. 01-UUN-2000; 2000US-0208538P. 30-OCT-2000; 2000US-0244989P.

(UYDE ) UNIV DELAWARE

Rice MC

Gamper HB,

Kmiec EB,

4PI; 2001-639230/73.

Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical

Claim 7; Page 208; 294pp; English. modification.

The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, cretinoblastoma, BRCAL, BRAZ, CFTR, cyclin-dependent kinase inhibitor 2h retinoblastoma, BRCAL, BRAZ, CFTR, cyclin-dependent kinase inhibitor 2h (CDRN2A), APC, Factor VIII, Factor IX, haemoglobin alpha locus (CDRN2A), haemoglobin alpha locus 2 (HBAZ), MLH1, MSH2, MSH6, apolipoprotein E (APOE), iDL receptor (LDLR), UDP-glucuronosyltransferase (UGTI), amyloid precursor protein (APC), presentin-1 (PSEN1) and presentilin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemomer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention 

Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Gape . Score 7.6; DB 1; Length 17; Pred. No. 5.2e+02; 4; Indels 0; Mismatches Query Match
27.1%;
Best Local Similarity 71.4%;
Matches 10; Conservative (

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6 CCTACGTGTACAGG 19 ccrccrccacaa

8

; 0

RESULT 615 ABA80104

ABA80104 standard; DNA; 17 BP

ABA80104;

(first entry) 24-JAN-2002 HBA2 mutation correcting oligonucleotide SEQ ID NO: 2950.

Human, gene therapy, adenosine deaminase deficiency; p53; beta-globin, retinoblastoma, BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma, APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VI; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOB; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UG71; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; altilipemic; ss.

Homo sapiens.

WO200173002-A2.

04-OCT-2001.

27-WAR-2000; 2000US-0192176P. 27-WAR-2000; 2000US-0192179P. 01-JUN-2000; 2000US-0208538P. 30-OCT-2000; 2000US-0244989P. 27-MAR-2001; 2001WO-US009761. 

(UYDE ) UNIV DELAWARE

Rice MC Gamper HB, Kmiec EB,

WPI; 2001-639230/73.

Oligonucleotide for targeted alterations of genetic sequences and for

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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of ganomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-aglobin, the following genes: adenosine deaminase, p53, beta-aglobin, action larged at crinoblastoma. BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A (CDKN22), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus. (HMA1), haemoglobin alpha locus. (HMA2), hamaly MA4, MA41, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New gene encoding a protein having ethanolaminephosphate cytidyltransferase activity, useful for treating Zellweger's syndrome, or lipid-related diseases such as cardiovascular diseases and obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse, ethenolaminephosphate cytidilyl transferase; ET; ds; splice donor site, antilipemic; cardiant, anorectic; phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease; cardiovascular disease; atherosclerosis; obesity.
treating cystic fibrosis, comprises at least one mismatch and chemical modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a mouse gene encoding a protein having ethanolaminephosphate cytidyltransferase (FT) activity appearing as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

27.1%; Score 7.6; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse ET gene 5' splice donor site from intron 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                Claim 7; Page 208; 294pp; English
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(POLO/) POLOUMIENKO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-844457/78.
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ö AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer. ADD71226, a degenerate variant of the ET gene, or a sequence that hybridises to the complement of the ET gene under stringent conditions. Also included is a promoter of a human ethanolaminephosphate cytidyltransferase gene appearing as ADD71227. The gene and promoter are useful for producing a transgenic animal, and for identifying, preventing, and treating diseases (by gene therapy) related to inappropriate phosphatidylethanolamine production, e.g. zellweger's syndrome, or lipid-related diseases auch as cardiovascular diseases, atheroscierosis and obesity. The present sequence is a mouse ET gene 5' splice donor site. Gaps Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss. . 0 Metastatic breast tumour cell upregulated transcript tag #3120. 26.4%; Score 7.4; DB 1; Length 10; 88.9%; Pred, No. 3.3e+02; ive 0; Mismatches 1; Indels Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other; Claim 1; Page 142; 219pp; English. 98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. AAZ83886 standard; DNA; 10 BP. 99WO-US013647 Query Match
Best Local Similarity 88.9%,
Best Active
Since 8, Conservative (first entry) Roberts BL, Shankara S; 14 TACAGGGAG 22 (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S. TACAGGTAG 9 WPI; 2000-106079/09. Homo sapiens. W09965928-A2 18-JUN-1999; 07-APR-2000 19-JUN-1998; 19-JUN-1998; 23-DEC-1999. 19-JUN-1998; 19-400-1998; AAZ83886; RESULT 617 AAZ83886/c 8888888888888 ઠે 셤

Gaps

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamontated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression the yeast gene is a candidate antifungal drug; (3) a method (M3) for
Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells e.g. cytotoxic I lymphocytes, and these used for adoptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannocated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
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                                                                                                                                                                                                                                                                          Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 164; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF37857 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                      9 ACGTGTACA 17
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Best Local Similarity
Matches 8; Conserv
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identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cyeast cell omprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 cepted and for identification of antifungal drugs. AAF33268 to AAF44064 cepted which in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF59989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99980, ABH00010-ABF9980, ABH00010-ABF99980, ABF99980, ABF99980, ABF99980, ABF99980, ABF99980, ABF99980, ABF99980, ABF99980, ABF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 273571 for detecting SNP TSC0003234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7.4; DB 1; Length 10;
Pred. No. 3.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABH73586 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.4%;
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Best Local Similarity 88.9
Matches 8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200177384-A2.
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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                               Oligonucleotide primer SEQ ID NO 323349 for detecting SNP TSC0031342.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 323349; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                               07-APR-2000; 2000DE-01019173.
                                                                                                                                                                                                                                                                                  06-APR-2001; 2001WO-IB000713
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              ABI23376 standard; DNA;
                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                        WO200177384-A2.
                                                                                                                                                                                             Homo sapiens
                                                                       22-FEB-2002
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                                          ABI23376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of an antisense oligonucleotide to the chick nerve growth factor receptor (NGFR) gene which was used as a control for the survival of mouse dorsal root ganglial (DRG) cells treated with oligonucleotides AAA887641-2. These oligonucleotides are antisense sequences directed at down-regulating the expression of the gene encoding the mouse p75 NGFR gene. The oligonucleotides can be used in methods to treat neurodegenerative conditions associated with disease and/or trauma such as Altheimer's, Parkinson's or Hungtington's disease, multiple sclerosis, vascular ischaemia associated with stroke, etc
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                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide; antisense; down-regulation; expression; trauma; nerve growth factor receptor; neurodegenerative disease; Alzheimer's; Parkinson's; Hungtington's disease; multiple sclerosis; vascular ischaemia; stroke; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti:sense oligo:nucleotide(s) to nerve growth factor receptor gene -
p75 NGFR, down-regulate expression and enhance neurone survival; for
treating cerebal palsy, Alzheimer's disease, stroke, etc.
                                                                                                       Gaps
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26.4%; Score 7.4; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 5.8e+02;
Matches 11; Conservative 0; Mismatches 6; Indels
                                                                     Query Match 26.4%; Score 7.4; DB 1; Length 12; Best Local Similarity 88.9%; Pred. No. 4.1e+02; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   Chick antisense oligonucleotide to p75 NGFR gene.
                                             Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 35; 59pp; English.
                                                                                                                                                                                                                                           AAQ87648 standard; DNA; 18 BP.
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                    8 TACGIGIAC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABF0010-ABF9989 and ABI0010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; se; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 273569 for detecting SNP TSC0003234.
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 75.v.
9; Conservative
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RESULT 621

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ41530;
                                                                                                                                                                                                                                                                                   Query Match
                     Inoue T;
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Matches
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                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amplification; polymerase chain reaction; PCR; microorganism; compost; detection; pollutant; soil; food; agricultural chemical; polymer; organochlorine; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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13
                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                             Claim 1, SEQ ID NO 273569; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.7%; Score 7.2; DB 1; Length 12; Best Local Similarity 75.0%; Pred. No. 4.6e+02; Matches 9; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Organic material detecting primer 107.
                                                                                                                           Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ41746 standard; DNA; 12 BP.
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99JP-00069694.
                                                             06-APR-2001; 2001WO-IB000713.
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                                                                                 07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                          Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ceracaceraca 1
                                                                                                     (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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                     WO200177384-A2
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  Homo sapiens.
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21-JAN-2000
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                                        18-OCT-2001
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This invention describes a novel method for the amplification of DNA comprising (i) preparing many primers (P) with different probabilities of amplification and (ii) simultaneous polymerase chain reaction (PCR) of different DNA using these primers. The method is used (i) to differentiate between different microorganisms in a mixed population and (ii) to determine presence/absence of an impurity (pollutant), or its concentration, in e.g. soil, foods, compost etc., typically metals, agricultural chemicals, polymers, organochlorine compounds etc. A particular use is monitoring composting of organic material. Amplification with many primers produces a lot of information, so reliability of the test is improved, and many samples may be tested quickly. AAZ1640-Z41855 represent the primers described in the method of the invention. (Updated on 20-WAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbe detection in organic waste arbitrarily primed PCR primer #107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Novel polymerase chain reaction method, for differentiating between microorganisms and for detecting contaminants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.7%; Score 7.2; DB 1; Length 12; 75.0%; Pred. No. 4.6e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
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(NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
                                                                                                                               Example 1; Page 19; 78pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 9; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ41530 standard; DNA; 12 BP
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This invention relates to a method for amplifying a DNA fragment. The method comprises successive repetitions of heat-denaturing, annealing of a primer and an extending step using a DNA polymerase. The method makes use of a cDNA pool in which the primer is one primer or a pair of primer sets and has an amplification probability which allows it to amplify a pNA fragment from a limited number of the cDNA among the DNA pool (where the limited number are anged of 1 to 25). Also included in the invention are apparatus used for carrying out the method, a primer and a bNA polymerase and a kit used for amplifying a DNA fragment. The method can be used to amplify a limited number of cDNAs from a pool in which a wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
extending step, to amplify the DNA fragments of a plural of different DNAs. The method can detect the existence of a microbe in organic waste. AAZ41424 to AAZ41639 represent PCR primers used in random amplified polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer used to illustrate DNA amplification method SEQ ID 107.
                                                                                                                                         Score 7.2; DB 1; Length 12; Pred. No. 4.6e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amplification of a DNA fragment and its apparatus
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                                                                                                           Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAOL ) SANYO ELECTRIC CO LTD.
(NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer; amplification; selective; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 9; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                              ВР.
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                                                                                                                                           Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                              AAC97881 standard; DNA; 12
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                                                                            organic waste
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The coligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 273565 for detecting SNP TSC0003234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 273565; 29pp + Sequence Listing; German.
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Matches 9; Conservative
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25.7%; Score 7.2; DB 1; Length 12; 75.0%; Pred. No. 4.6e+02; tive 0; Mismatches 3; Indels

9; Conservative 11 GTGTACAGGAG 22 1 GAGTACACGAAG 12

Local Similarity

Query Match

Best Loca Matches

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Berlin K;

Berlin K;

Olek A, Piepenbrock C,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI32073 data for this patent did not form part of the printed specification, but the obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 230559; 29pp + Sequence Listing; German.
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Best Local Similarity 75.0
Matches 9, Conservative
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                                                                                                                                                                                                                                                                              designed to detect methylation status.
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                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                  oet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  25.7%; Score 7.2; DB 1; Length 13; 75.0%; Pred. No. 5e+02; 2ive 0; Mismatches 3; Indels
                                                                                                                                    Claim 1; SEQ ID NO 62988; 29pp + Sequence Listing; German.
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ABC62970 standard; DNA; 13 BP.
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25.7%; Score 7.2; DB 1; Length 13; 75.0%; Pred. No. Se+02; tive 0; Mismatches 3; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at
oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF000010-ABF9989, ABF00010-ABF9989, ABF000010-ABF9989, 
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DB 1; Length 13;

25.7%; Score 7.2;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for derecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                 ö
                                                                                                                                                                                                                                                               Oligonucleotide SEQ ID NO 62985 for detecting SNP TSC0016657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7%; Score 7.2; DB 1; Length 13; 75.0%; Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 62985; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3, Indels
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВЪ.
                                                                                                                                                               ABC62968 standard; DNA; 13 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-2000; 2000DE-01019173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2001; 2001WO-IB000713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABH30583 standard; DNA; 13
                                                                                                                                                                                                                                 21-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
Best Local Similarity 75.(
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TACGTGTACAGG 19
                                               8 TACGTGTACAGG 19
                                                                             TACCTCTACACG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 designed to detect methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  WO200177384-A2.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2001.
                                                                                                                                                                                                 ABC62968;
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                                                                                                                                 RESULT 631
                                                                                                                                                 ABC62968/
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WO200022111-A1.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH0010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                           Oligonucleotide SEQ ID NO 230560 for detecting SNP TSC0056234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 230560; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was obtained in electronic format from WI
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin K;
                                                                                                                                                                                                                                                                                              36-APR-2001; 2001WO-IB000713
                                                                                                                                                                                                                                                                                                                                      07-APR-2000; 2000DE-01019173
                     22-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-657177/75
                                                                                                                                                                                                                  WO200177384-A2.
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                          18-OCT-2001.
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0; Gaps / Match 25.7%; Score 7.2; DB 1; Length 13; Local Similarity 75.0%; Pred. No. 5e+02; hes 9; Conservative 0; Mismatches 3; Indels Query Match Best Loca Matches

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10 CGTGTACAGGGA 21

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AAA52434 standard; DNA; 15 BP. AAA52434; RESULT 633 

Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M; 1gM; V gene diversity; directed constitutive hypermutation; target sequence diversification; terminal deoxynucleotidyl transferase; TdT; clonal expansion; selection; heavy chain variable region; VH;

Homo sapiens Synthetic. mutant; ds.

IdT-expressing Ramos cell VH insertion+deletion mutation, F264. 18-SEP-2000 (first entry)

The invention relates to a method of preparing a lymphoid cell line capable of directed constitutive hypermutation of a target moleic acid region. The method comprises screening a cell population for mucleic acid region. The method comprises screening a cell in which the rape of target mucleic acid mutation exceeds that of other nucleic acid mutation or more. The invention also relates to a method for preparing a gene product with a desired activity, comprising expressing a nucleic acid encoding the target gene operably linked to a method for preparing a gene product with a desired activity, comprising expressing anticleic acid encoding the target gene operably linked to a method for preparing of the invention e.g., terminal decoxymucleotidyl transferase (TdT), in the lymphoid cell line, and identifying a cell or calls which express a mutated gene product with the desired activity. Colls which an improved activity of interest are selected. These steeps may be iteratively repeated until a gene product with a desired of activity is obtained. The cell lines prepared according to the method of the cinvention are used for directed constitutive hypermutation of a nucleic acid region in the preparation of a gene product, preferably an enzyme or immunoglobulin (Ig) with a desired activity. In the exemplifications of the invention, Ighs secreting Ramos cells were selected for use as they undergo hypermutation during clonal expansion. This was determined on the basis of the amount of diversity in the heavy chain variable region (VH). Sequences AAA5236+2434 represent fragments of Ramos cells with a corresponds. Sequences AAA52389+A52434 represent mutations that corrur in Ramos cells which express IdT, and sequences AA5236-A52487 regreent mutations that courr in non-IdT- expressing control Ramos cells with a desired during control Ramos cells with a sequence and activity of mutations that occur in non-IdT- expressing control Ramos cells Lymphoid cell line preparation useful for producing gene products having desired activity, involves screening and selecting cells having ongoing target sequence diversification and higher mutation rates. 25.7%; Score 7.2; DB 1; Length 15; 75.0%; Pred. No. 5.6e+02; ive 0; Mismatches 3; Indels Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other; Neuberger MS, Cumbers SJ; Example 4; Fig 6; 69pp; English 99WO-GB003358 99GB-00001141, 98GB-00022104 Best Local Similarity 75.0%; Matches 9; Conservative (MEDI-) MEDICAL RES COUNCIL AAZ62686/c ID AAZ62686 standard; RNA; 15 28-MAR-2000 (first entry) 11 GTGTACAGGGAG 22 3 GTGCACATGGGG 14 WPI; 2000-317971/27 08-OCT-1999; 19-JAN-1999; 09-OCT-1998; 20-APR-2000 Sale JE, AAZ62686; Query Match RESULT 634 à CXXXXXXXX

Substrate for HH ribozyme HCV-5596 which cleaves HCV RNA at

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99US-00274553 99US-00274553

23-MAR-1999; 23-MAR-1999;

27-JUN-2002.

US2002082225-A1.

MCSWIGGEN J A. ROBERTS B. PAVCO P A.

(BLAT/) (MCSW/) (ROBE/)

(PAVC/) PAVCO P A. (MACE/) MACEJACK D.

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The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the hepatitis of virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme series were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the target the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatotellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune diseases, and cancer
Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer; autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme; HCV expression, HCV replication, cirrhosis, virucide, liver failure, hepatocellular carcinoma, HCV infection, drug therapy, type I interferon, interferon alpha, interferon beta, cytostatic; interferon gamma, consensus interferon, hepatotropic; antiinflammatory, substrate, hammerhead ribozyme, HH ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                           Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus substrate #319 for HCV hammerhead ribozyme #319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.7%; Score 7.2; DB 1; Length 15; Best Local Similarity 75.0%; Pred. No. 5.6e+02; Matches 9; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                       Pavco PA, Macejak D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                       Mcswiggen JA, Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 59; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABX00537 standard; RNA; 15 BP.
                                                                                                                                                                                                                    98US-0083217P.
98US-0100842P.
99US-00257608.
99US-00274553.
                                                                                                                                                                                    99WO-US009027
                                                                                                                                                                                                                                                                                                                 (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 ACAGGGAGTCCA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 ACCTGGACTCCA 2
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-062023/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus
                                                                         Hepatitis C virus
                                                                                                                                                                                                                    27-APR-1998;
18-SEP-1998;
25-FEB-1999;
23-MAR-1999;
                                                                                                           WO9955847-A2.
                                                                                                                                                                                    26-APR-1999;
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                                                                                                                                                 04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                       Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX00537;
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ABX00537/c
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The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HEP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon. Sepecially interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic formet directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonamocated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.7%; Score 7.2; DB 1; Length 15; 75.0%; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11372.
                                                                                                                                                                                                                                                                  Roberts B, Pavco PA, Macejack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 30; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF43233 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 ACAGGGAGTCCA 26
                                                                                                                                                                                                                                                                  Blatt L, Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTGGACTCCA 2
                                                                                                                                                                                                                                                                                                WPI; 2002-617759/66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 636
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BXBXSXAMAXSXBXBXBXBXBXBXBXBX
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open redding frame; or nonamontated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering a NORF gene whose expression varies by at class, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance which seets the spast of cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguing expression in the yeast cell with a candidate drug as a member of contiguous nucleotides of a NORF gene whose expression is affected by the class of the cell cycle, the differentially contacting a yeast cell with a candidate drug and contacting a yeast cell of at least 1 NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. Apr3326 to AAP434064 crepresent SAGE tags used in the exemplification of fine present invention
                                                                                                                                                                                                                                                                         Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                               Jelculescu V, Vogelstein B, Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 356; 419pp; English.
                        14-JUN-2000; 2000WO-US016223.
                                                                         16-JUN-1999; 99US-00335032.
                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                             WPI; 2001-061874/07.
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25.0%; Score 7; DB 1; Length 10; 100.0%; Pred. No. 4e+02; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.,

19 GGAGTCC 25 α

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RESULT 637

AAF36719 standard; DNA; 10 BP. 

23-MAR-2001 (first entry)

AAF36719;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3458.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle; NORF; nor previously assigned open reading frame, nonannotated ORF; SAGB, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

Homo sapiens

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a sAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drug comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a cut (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cut (4) a method in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle. The expression is affected by the class of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle. The cycles and for identification of antifungal drugs, the differentially expression is affected as markers of phases of the cell cycle. The cycle and for identification of antifungal drugs, which affect the cell cycle are paresent sAGE tags used in the exemplification of the present invention.

Appression the exemplification of the present invention.
                                                                                                                                                                                                                                                                                               Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human skin stress/ageing related EST SEQ ID NO 334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
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100.0%; Pred. No. 4e+
tive 0; Mismatches
                                                                                                                                                                                                                Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 123; 419pp; English
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                                                                                                                                                                                                                Velculescu V, Vogelstein B,
                                                                                 14-JUN-2000; 2000WO-US016223
                                                                                                                            16-JUN-1999; 99US-00335032
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                                                                                                                                                                   (UYJO ) UNIV JOHNS HOPKINS.
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Best Local Similarity 100..
Lagary 7; Conservative
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WO200077214-A2
                                       21-DEC-2000
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGRACYNNYTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-S0925 represent specific examples of probe sequences used in the search. Autibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are
                                                                                                                                    The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaais; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; scasca, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.0%; Score 7; DB 1; Length 11;
100.0%; Pred. No. 4.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemopoietin receptor family; NRB; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
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                                                                                                   Disclosure; Page 102; 1345pp; German.
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98JP-00297409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmacoutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                         Identifying genes involved in skin stress and aging, useful e.g. in
screening for cosmetic or therapeutic agents, based on differential gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                 Hofmann
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                                                                                                      20-DEC-2001; 2001WO-EP015178.
                                                                                                                                                     03-JAN-2001; 2001DE-01000121.
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                                                                                                                                                                                                                                                 Petersohn D, Conradt M,
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                                                                                                                                                                                               (HENK ) HENKEL KGAA
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Hofmann K;

Petersohn D, Conradt M,

WPI; 2002-590638/63

(HENK ) HENKEL KGAA

ABV64991;

RESULT 639

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Gaps

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RESULT 641

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AAZ90834 ID AA70

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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a muchiet acid database with the nucleic acid probe sequence TGGAGYNNWTGGAGY encoding the amino acid sequence TTP_Ser.Kaa TTP_Ser. The sequences AAZ59258-Z59300 and AAZ90816-Z9025 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.0%; Score 7; DB 1; Length 15; 100.0%; Pred. No. 6e+02;
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blood formation disorder; fusion protein; probe; ss.
                                                                                                      NR8; antibody; diagnosis;
                                                                                                        Haemopoietin receptor family, NR8; antibody; diagnos
blood formation disorder; fusion protein; probe; ss.
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98JP-00297409
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                                   (first entry)
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Best Local Similarity 100.
Matches 7; Conservative
                                                                       Human NR8 gene probe #113
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                                                                                                                                                                                                                                                                                                                                                                                                         Nomura H, Maeda M;
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                                                                                                                                                                  Homo sapiens
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19-OCT-1998;
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                                   24-MAY-2000
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AAZ90885;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNYTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90316-Z90925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders
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                                                                                                              Gaps
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                                                                       25.0%; Score 7; DB 1; Length 15; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
                                     Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
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 used for the treatment of such disorders
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98JP-00297409
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Best Local Similarity 10v...
7; Conservative
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                                                                         Query Match 25.0
Best Local Similarity 100.
Matches 7, Conservative
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19-OCT-1998;
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99WO-JP003351

23-JUN-1999;

AAZ90885 standard; DNA; 15

AAZ90885 ID AAZ9 XX

RESULT 642

Mon Apr 19 15:55:12 2004

98JP-00214720. 98JP-00297409.

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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGRAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59288-Z59300 and AAZ90816-250928 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse scavenger receptor class B type 1 oligonucleotide SEQ ID NO:275.
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                                                                                                                                Hemopoietin receptor protein family NR8 used for diagnosis of blood
                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
                                          (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC
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                                                                                                                                                                                                                                                                                                                                      used for the treatment of such disorders
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                                                                                                                                                                                   Example 1; Page 45; 176pp; Japanese
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15-JUN-2001; 2001US-00212308
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                  formation disorders
                                                                        Maeda M;
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24-JUN-1998;
19-OCT-1998;
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AAA11707-A11710 represent the PCR primers described in the method of the
  The present invention describes a method for identifying oligonucleotides with desired hybridisation properties to nucleic acid trargets containing accondary structure. The method comprises amplifying a target nucleic acid having at least one accessible and one inaccessible site. Primers that form an extension product are identified as the oligonucleotides which can interact with the folded target nucleic acid. Oligonucleotides from the present invention can be used in novel detection methods for clinical diagnostic purposes, including the detection methods for of pathogenic organisms (e.g. HIV). The method allows the ability to rapidly analyse mucleic acid structures. ABL46034 to ABL46367 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate-specific antigen; PSA; detection; prostate cancer; PCR primer;
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A primer DNA and detection of an mRNA encoding a prostate-specific antigen by using it.
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25.0%; Score 7; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
Matches 10; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                        25.0%; Score 7; DB 1; Length 17; 66.7%; Pred. No. 6.4e+02; Live 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                       Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate-specific antigen PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HITB ) HITACHI CHEM CO LTD.
(NIID-) NIPPON IDENSHI KENKYUSHO KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA11710 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                   15 GTAGACATAGGGTCC 1
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Best Local Similarity 66.7
Matches 10; Conservative
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25.0%; Score 7; DB 1; Length 15; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels

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rng.res

8 TACGTGTACAGGGAG 22

19 rcccrcrackáczaká s

AAF38150 standard; DNA; 10 BP

AAF38150;

(first entry) 23-MAR-2001

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4889.

nor previously assigned open reading frame; nonamotated ORF, SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223

16-JUN-1999;

99US-00335032

SNINGOH SNHOL VINU ( OLYU)

Jelculescu V, Vogelstein B, Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 174; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) for using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, 5 phase and G2/M; (2) a method (M2) for screening candidate of cell; and (b) monitoring expression of a test substance with a yeast cell; and (b) monitoring expression of a whore a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying a candidate antifungal drug; (3) a method (M3) for identifying a candidate antifungal drug; (3) a method (M3) for identifying a candidate drug as member of comprising contacting a yeast cell with a candidate drug and mod (4) a method (M4) for identifying a candidate drug as member of class of drugs having a characteristic effect on gene expression in a yeast cell omprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene may be used contacting a yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used as well affect phases of the cell cycle. The methods may be used as markers of phases of the cell cycle of cycle and for identification of antifungal drugs. Affaltion of the present invention. AMF33262 to AAF33267 represent linkers and the present invention. 

Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match

24.3%; Score 6.8; DB 1; Length 10;

ö Gaps ö Indels Pred. No. 4.5e+02; 0; Mismatches 2; 80.08; 8; Conservative 8 TACGTGTACA 17 Best Local Similarity Matches δ

recereraca 10

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RESULT 647 AAF40202

AAF40202 standard; DNA; 10 BP

AAF40202;

23-MAR-2001 (first entry)

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6941.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

16-JUN-1999; 99US-00335032.

SNIXGOH SNHOL VINU ( OLYU)

Kinzler K; Vogelstein B, Velculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 247; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at clast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of antifungal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying a condidate drug as a member of a comprising contacting human DNA with a probe which comprises at least 10 comprising contacting a yeast cell with a candidate drug and class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle. The contioning expression in the yeast cell of at least 1 NORF gene may be used to study, monitor and affect phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. The NORF gene and seed to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs of the cell cycle. The methods may be used in the exemplification of the present invention.

Cycle and the exemplification of the present invention of the present invention.

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; ichthyosis; malanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                 Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 289277 for detecting SNP TSC0013867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.3%; Score 6.8; DB 1; Length 11; 80.0%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels
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                 21-OCT-2002 (first entry)
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Best Local Similarity 80.0.
Set Local 8 Conservative
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                                                           Human skin EST 6247.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from expression. (A) comprises protein or mRNAs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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                                       24.3%; Score 6.8; DB 1; Length 10; llarity 80.0%; Pred. No. 4.5e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Human skin stress/ageing related EST SEQ ID NO 102.
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Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 41; 325pp; German.
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Best Local Similarity 80.07
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es 8; Conserv
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WO200177384-A2

ABV68461

ABV68461 ID ABV6 XX AC ABV6

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18-OCT-2001,

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Set of oligonuclectides, useful for diagnosis and cell typing, is
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                                                                                                                                                                                   Local Similarity 80.0 es 8; Conservative
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                                         Olek A, Piepenbrock C,
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                              (EPIG-) EPIGENOMICS AG
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Matches
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99899, ABF00010-ABE99899, ABF00010-ABE99899, ABF00010-ABE99899 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitte. Wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                          Claim 1; SEQ ID NO 276700; 29pp + Sequence Listing; German
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Best Local Similarity 80.00,
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                              methylation status.
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  ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                        oet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 289277; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was obtained in electronic format from Wl
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                          Berlin K;
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                                                 06-APR-2001; 2001WO-IB000713.
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AAV11115 standard; RNA; 13

AAV11115;

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Gaps

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2 CCTACACGTA 11

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 310676 for detecting SNP TSC0024049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                  24.3%; Score 6.8; DB 1; Length 12; llarity 80.0%; Pred. No. 5.5e+02; Conservative 0; Mismatches 2; Indels
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                                                                                              Seguence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                      ABI10703 standard; DNA; 12 BP,
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Best Local Similarity
Matches 8; Conserv
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AAV10915-V11123 are target sequences for a novel ribozyme which cleaves specific alleles from the major histocompatability complex (MHC). This ribozyme contains a catalytic region and a hybridisation region which is complementary to all mRNA transcribed from vertebrate genes of a specific family of closely related MHC alleles or to mRNA from a single MHC allele, and is able to cleave such mRNA. The mRNA has a target region which in case is essentially conserved in all genes of the family but differs from genes of all other MHC alleles to such a degree that no cleavage of mRNA transcribed from these other alleles occurs. This allows the selective reduction or inhibition of expression of all genes of a family or of a single gene. This ribozyme can be used for permanent or transfert suppression of Expression of MHC alleles, in vivo or in vitro. Specific applications are to prevent guest vs. host or host vs. guest reactions, to prevent blood incompatibilities (partic. of the ABO rhesus and theumatoid arthritis. The use of this ribozyme avoids the need for immunosuppressants in transplant patients. It provides very between donor and recipient. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft versus host reactions, to overcome blood incompatibility and to treat auto:immune disease.
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major histocompatablity complex; cleavage; suppression; transplant;
incompatibility; autoimmune disease; juvenile diabetes;
rheumatoid arthritis; ss.
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                                                                                                                                             Human ribozyme target sequence from HLA-DRB 19DRB #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MARG/) MARGET M.
(WEST/) WESTPHAL E.
(MUEL/) MUELLER-RUCHHOLTZ W.
                                                                                       (revised)
(first entry)
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                                                                                                                                                                                                                                                                              Homo sapiens.
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Gaps

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Query Match 24.3%; Score 6.8; DB 1; Length 12; Best Local Similarity 80.0%; Pred. No. 5.5e+02; Matches 8; Conservative 0; Mismatches 2; Indels

6 CCTACGTGTA 15

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This invention describes novel oligonuclectide primers or peptide nucleic acid (FNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF0010-ABF99989, ABH0010-ABF99989 and ABI0010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Matches 8; Conservative
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                                                                                                  Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 targement the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 9230 for detecting SNP TSC0002450.
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                                                                                                               ABC09239 standard; DNA; 13 BP.
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12 CCGGGATTCC
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Matches
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RESULT

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98US-0082404F.

20-APR-1998; 23-JUN-1998;

Bellon L;

Karpeisky A, Haeberli P;

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with a target sequence and contain at least one phosphoro (dithioate link, having endonuclease activity. (A), and more generally any catalytic link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the obsertogen receptor gene, are used to treat cancer (particularly of breast or endometrium).

In vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor.

Correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA2444 represent cestrogen receptor hairpin ribozyme sequences, and AAA2593 to AAA2618 represent their corresponding target sequences, and AAA2619 to AAA2621 to AAAA2611 to Expresent other ribozyme sequences and entered of the present of the present of the present contents of the 
                                                                                                                                                                                                                                                                        New nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                            present invention describes nucleic acids (A) that interact stably
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                                                                                                                      Beigelman L, Mcswiggen JA, Zwick M, Jarvis T, Woolf T,
                                                                                                                                                                                                                                                                                                                                               Claim 79; Page 98; 148pp; English.
                                                                       (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                  used to treat cancer.
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                                                                                                                    Thompson JD, Beig
Reynolds M, Zwick
Matulic-Adamic J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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10-JAN-2002. ö c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense; phosphorothioate; ss. Gaps ö Score 6.8; DB 1; Length 14; Pred. No. 6.2e+02; 0; Mismatches 2; Indels (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK. c-fos antisense oligonucleotide. AAQ83430 standard; DNA; 14 BP. 24.3%; 94WO-EP002218 93EP-00111059 (first entry) Local Similarity 80.0 les 8; Conservative 10-JUL-1993; 409502051-A2 19-JAN-1995

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated human electron-transfer-flavoprotein, beta polynucleotide, useful for therapeutic purposes, for studying the expression and function of the polynucleotide, and for expressing the flavoprotein.
                                                                                  Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and treating neuronal injury, degeneration, cell death and/or neoplasms.
                                                                                                                                                                  Antisense nucleic acid hybridising with an area of the mRNA and/or DNA comprising the genes c-jun, jun-B or c-fos, expression of which plays a causal role in neuronal injury, degeneration, cell death and/or neoplasms, can be used to prevent and treat such conditions. c-jun antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B antisense sequences are described in AAQ83367-33 and AAQ83444-45; and c-fos antisense sequences are described in AAQ83364-439 and c-free apply the antisense sequences are phosphorothioate oligonucleotides since these are not destroyed as fast by endogenous factors as naturally occuring molecules. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises DNA, cDNA and protein sequences of the human electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on chromosome 19q13.3-13.4). The invention specifically relates to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, electron-transfer flavoprotein beta polypeptide; ETFB;
electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
novel polymorphic aite; novel polymorphism; ETFB genotype; 88; GAII;
ETFB haplotype; transgenic animal; primer; probe; chromosome 19013;
primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
             Brysch W
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                24.3%; Score 6.8; DB 1; Length 14; 80.0%; Pred. No. 6.2e+02; tive 0; Mismatches 2; Indels
             Schlingensiepen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ETFB allele-specific oligonucleotide primer 24.
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
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               Schlingensiepen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 14; 143pp; English.
                                                                                                                                           Claim 2; Page 65; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentivegna SC, Bieglecki KM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2001; 2001WO-US021306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GTGTACAGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GTATACAGAG 13
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                                                   WPI; 1995-066896/09.
               Schlingensiepen G,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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identification of 27 novel polymorphic sites within the ETFB gene.

Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
for nine primary flavoprotein dehydrogenases and is located in the
mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta

(ETFB) subunit. Electrons accepted by ETF are transferred to the
mitochondrial respiratory chain by ETF dehydrogenases (ETFBH).

Deficiency of ETF or ETFBH leads to glutaric acidaemia type II (GAII).

Therefore ETFB is a pharmaceutically important gene in the treatment of
CAII. The novel ETFB polymorphisms identified in the invention are useful
CAII. The novel ETFB polymorphisms identified in the invention are useful
CO genotyping and haplotyping the ETFB gene of an individual. The ETFB
protein and nucleic acids of the invention are useful for studying the
expression and function of ETFB in vivo. The ETFB protein and nucleic
acids are also useful for testing the efficacy of therapeutic agents and
compounds for glutaric acidaemia type II. The mucleic acids of the
invention are useful in the production of a transgenic animal expressing
the ETFB gene. Nucleic acids ABI3944+ABI3944 represent claimed
ETFB allele-specific probes. Nucleic acids ABI3944-ABI3944 represent claimed
ETFB allele-specific prox primers. Nucleic acids ABI3944-ABI3944 represent claimed
ETFB allele-specific prox primers. Nucleic acids ABI3944-ABI3944 represent claimed
ETFB allele-specific prox primers. Nucleic acids ABI3944-ABI3944 represent claimed
ETFB allele-specific prox primers. Nucleic acids ABI3944-ABI3944 represent claimed
ETFB allele-specific prox primers. Nucleic acids ABI3944-ABI3944 represent claimed
ETFB allele-specific prox primers. Nucleic acids ABI3944-ABI3944 represent claimed
ETFB allele-specific prox primers. Nucleic acids ABI3944-ABI3944 represent claimed
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ö 24.3%; Score 6.8; DB 1; Length 15; 80.0%; Pred. No. 6.4e+02; ive 0; Mismatches 2; Indels Query Match
Best Local Similarity 80.0
Matches 8; Conservative ઠ

В

RESULT 66
ABA03963
LD ABA03963
LD ABA03963
XX ABA03963

ABA03963 standard; DNA; 15 BP ABA03963;

19-FEB-2002 (first entry)

Human STK11 gene polymorphism detection ASO primer SEQ ID NO:30.

Human; STX11; serins/threonine kinase 11; polymorphism; SNP; single nucleotide polymorphism; Peutz-Jeghers Syndrome; genotyping; haplotype; genetic variant; haplotyping; allele-specific oligonucleotide; ASO; primer; ss.

Homo sapiens

WO200187906-A2

22-NOV-2001

17-MAY-2001; 2001WO-US016045.

17-MAY-2000; 2000US-0204697P.

(GENA-) GENAISSANCE PHARM INC.

Chew A, Choi JY, Nandabalan K, Sausker EA; WPI; 2002-055679/07. Bieglecki KM,

Novel genetic variants of serine/threonine kinase 11 (Peutz-Jeghers syndrome) useful in studying expression and function of the protein, and for screening candidate drugs to treat diseases e.g. Peutz-Jeghers

Claim 16; Page 13; 86pp; English.

syndrome.

The present invention describes a method for haplotyping the serkine/threonine kinase 11 (Peutz-Jeghers syndrome) (STKI1) gene of an individual. STK11 gene sequences can be used in gene therapy. The STK11 gene is useful for screening drug targeting comprising contacting STK11

with a candidate agent and assaying for binding activity. STX11 is useful discovery and development of drugs for treating diseases associated with STX11 activity, e.g. Peutz-Jephers syndrome. The method is useful for haplotyping the STX11 gene in an individual, which can also be used in haplotyping the STX11 gene in an individual, which can also be used in haplotyping the STX11 gene in an individual, which can also be used in haplotyping the STX11 gene in an individual, the can also be used in design of clinical trials of candidate drugs for, treating a specific condition drugs or disease predicted to be associated with STX11 and primers for assaying a polymorphism in the target region. The present sequence represents an ASO primer used for detecting STX11 gene nvention

886666666666666888

Sequence 15 BP; 2 A; 6 C; 6 G; 0 T; 0 U; 1 Other;

Gaps ô 24.3%; Score 6.8; DB 1; Length 15; 80.0%; Pred. No. 6.4e+02; tive 0; Mismatches 2; Indels Query Match
Best Local Similarity 80.07

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RESULT 661

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1767/c AAA51767 standard; DNA; 16 BP.

AAA51767;

31-OCT-2000 (first entry)

CYP3A5 gene 5' flanking region forward sequencing primer 3A5p01

CYP3AS; Cytochrome P450; transcription regulatory region; polymorphism; Activator protein-3 motif; AP-3; basic transcription element; drug metabolism; phenotype; sequencing primer; ss.

Homo sapiens.

WO200039332-A1.

06-JUL-2000.

99WO-GB004380. 22-DEC-1999;

98GB-00028619. 23-DEC-1998;

(JANC ) JANSSEN PHARM NV.

Paulussen ADC, Armstrong M;

WPI; 2000-452418/39.

Identifying subjects with a high drug metabolizing phenotype associated with cytochrome CYP3AS expression for establishing whether a drug will k metabolized by the subject.

Disclosure, Page 39; 68pp; English.

Cytochrome P450 subfamily CYP3A5 transcription regulatory regions can be screened for the presence/absence of a polymorphic variant, preferably at positions -475 or -147 of the DNA of the 5' flanking region adjacent to the CYP3A5 coding sequence. The variants are present in an activator protein-3 (AP-3) motif and/or a basic transcription element (BTE). The polymorphisms cause increased CYP3A5 gene expression and this has been linked to drug metabolic activity. Screening for the presence of variants can be used to identify subjects with a high or low drug metabolizing phenotype associated with cytochrome CYP3A5 expression. Primers are used which in addition to hybridizing to the site of interest, are capable of introducing a restriction site which is absent in either the wild type sequence or polymorphic variants. Restriction enzyme cleavage analysis 

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Gaps ò

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Microsatellite markers based on hypervariable genomic fragments, from Triticum aestivum (wheat) or the tribe Triticeae, consist of a sequence tagged site (STS), defined by 2 specific primers (of mean size 17-23 bases) that flank a microsatellite sequence at both ends, which can be amplified to polymorphisms (PCR products of different sizes). The microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri- or tetra-nucleotide sequences, combination microsatellite sequences or an imperfect sequence in which individual bases are mutated. The microsatellite markers can be used for genetic analysis of hexaploid and rerapploid forms of wheat and for genetic mapping or labelling of monogenic and polygenic properties, and for their selection; for analysing relationships and identifying varieties; and for evaluating varietal purity, hybrid identification and plant growth. The markers can differentiate between almost all Buropean wheat lines and show a higher degree of DNA polymorphism than known probes for the wheat genome. They can be detected by PCR, so large numbers of samples can be analysed can be detected by PCR, so large numbers of samples can be analysed casily (e.g. several hundred per day). Microsatellite marker-related polymorphisms are stably inherited so can also serve as genetic markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsatellite marker; hypervariable genomic fragment; Triticum aestivum; wheat; Triticeae; sequence tagged site; STS; primer; PCR; amplify; polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.
can then be used to indicate the presence or absence of the variant. The methods are used to establish, before treatment with a drug, whether the drug will be effectively metabolised by the patient, to identify compounds and transcription factors that can bind to a DNA sequence encoding CYPRAS, diagnosing susceptibility to a disease which is caused by toxins or procarcinogens metabolized by CYPRAS and for identifying mutagenic effects of a compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primers for STS micro:satellite markers for wheat and related species -useful for genetic mapping, analysis and labelling etc. of wheat.
                                                                                                                                                                                                                24.3%; Score 6.8; DB 1; Length 16; 80.0%; Pred. No. 6.6e+02; 1ive 0; Mismatches 2; Indels
                                                                                                                                                                            Sequence 16 BP; 6 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheat microsatellite WMS261 left primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roeder M, Plaschke J, Ganal M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 8; 8pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT77699 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1997 (first entry)
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Best Local Similarity 80.v
                                                                                                                                                                                                                                                                                                          7 CTACGTGTAC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT77699;
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is proteins and their coding sequences: MD23, MD24, MD212. MD212. MD23 is encoded at chromosome 7422.1, MD24 is encoded at chromosome 6921.3-222.2, MD27 is encoded at chromosome 16911.2 and MD212 is encoded at chromosome 16912.2 and MD212 is encoded at chromosome 16913.2 and MD212 is encoded at chromosome 1692. Treating or preventing a disorder secret manufacturing a medicament for treating or preventing a disorder or 15926. The manufacturing a medicament for treating or preventing a disorder or 250 mD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic, immunostimulant, gene therapy, vaccine, human, zinc finger protein, MD21, MD21, MD212, chromosome 7q22.1, chromosome 6p21.3-22.2, chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                              Gaps
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0
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                                                                           Length 19
                                                                                                              2; Indels
microsatellite markers. WMS261 has a CT type repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;
                                 Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                           Human MDZ3 scanning oligonucleotide SEQ ID 2838.
                                                                      Score 6.8; DB 1;
Pred. No. 6.7e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                           ADB01852 standard; DNA; 25 BP
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                                                                        24.3%;
80.0%;
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                                                                                           Similarity 80.08; Conservative
                                                                                                                                                      7 CTACGIGIAC 16
                                                                                                                                                                                           1 CTCCCTGTAC 10
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                                                                           Query Match
Best Local S
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ADB01852/c
                                                                                                                  Matches
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Gaps

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AAV10915-V11123 are target sequences for a novel ribozyme which cleaves specific alleles from the major histocompatability complex (MHC). This cribozyme contains a catalytic region and a hybridisation region which is complementary to all mRNA transcribed from vertebrate genes of a specific allele, and is able to cleave such mRNA. The mRNA has a target region which in case is essentially conserved in all genes of the family but differs from genes of all other MHC alleles to such a degree that not cleavage of mRNA transcribed from these other alleles occurs. This allows the selective reduction or inhibition of expression of all genes of a family or of a single gene. This ribozyme can be used for permanent or transient suppression of expression of MHC alleles, in vivo or in vitro. Specific applications are to prevent guest vs. host or host vs. quest reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus with the standard and to treat autoimmum diseases such as juvenile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes and rheumatoid arthritis. The use of this ribozyme avoids the need for immunosuppressants in transplant patients. It provides very specific reduction of particular HLA molecules that cause incompatibility between donor and recipient. (Updated on 25-MAR-2003 to correct PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft versus host reactions, to overcome blood incompatibility and to treat
                                                                                                                                                                                                                                                                                                Ribozyme; target; human lymphocyte antigen; HLA-DPB; MHC allele;
major histocompatability complex; cleavage; suppression; transplant;
incompatibility; autoimmune disease; juvenile diabetes;
rheumatoid arthritis; sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.6%; Score 6.6; DB 1; Length 13; larity 69.2%; Pred. No. 6.3e+02; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krupp G, Marget M, Westphal E, Mueller-Ruchholtz W;
                                                                                                                                                                                                                                                               Human ribozyme target sequence from HLA-DPB 02DPB #3.
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5 CCCTACGTGTACAGGGAG 22
                                   25 cacrecrecacacaras 8
                                                                                                                               AAV11022 standard; RNA; 13 BP
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                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           auto:immune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRUPP G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                WO9704087-A1.
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                     25-MAR-2003
14-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1997.
                                                                                                                                                                 AAV11022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUEL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRUP/)
                                                                                                           AAV11022,
                                                                                         RESULT
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligomuclectide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present equence is an oligomuclectide which can be used to design the antisense oligomuclectides of the present invention (see AAF$151 and AAF$153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, blaris, serborthoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovacular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, hyperproving the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 6.6; DB 1; Length 15;
Pred. No. 6.9e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 3 A; 9 C; 1 G; 2 T; 0 U; 0 Other;
                                                              Example 7; Page 53; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 CCCTACGTGTACA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cacrececined 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 69.2
Matches 9; Conservative
inflammation.
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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

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Gaps

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Best Local Similarity
Matches 9; Conserv

to correct PI field.)

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Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin disorder, Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding procein, IGFBP-2; IGFBP3; inflammation, psoriasis; pitaris, growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba, keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasis, kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                     Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                 (MURD-) MURDOCH CHILDRENS RES INST.
                                                                    BP
                                                                                                                               IGFBP3 oligonucleotide #1373.
                                                                                                                                                                                                                                                                                                                            99US-0140345P.
                                                                                                                                                                                                                                                                                                          21-JUN-2000; 2000WO-AU000693
                                                                   AAF47953 standard; DNA; 15
                                                                                                            (first entry)
9 ACGTGTACAGGGA 21
                                                                                                                                                                                                                                                                                                                                                                    Wraight CJ, Werther GA,
                  13 ACTGGTACACGTA 1
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-041421/05.
                                                                                                                                                                                                                                                                  WO200078341-A1.
                                                                                                                                                                                                                                                                                                                             21-JUN-1999;
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                            30-MAR-2001
                                                                                                                                                                                                                                                                                    28-DEC-2000.
                                                 RESULT
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08-MAY-1996 (first entry)
심
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The cDNA sequences encoding several multiple tumour suppressor (WTS) polypeptides have been isolated and sequenced, using various sequencing and amplification primers. The primer represented in this sequence was used to distinguish between two different promoters of MTS1, one alphaspecific and one beta-specific. MTS polypeptide-encoding cDNAs and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing predisposition to melanoma, leuksemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, astrocytoma, glioblastoma, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells contg. an altered MTS gene are useful for screening for potential cancer
                                                                                                                                                                                                                                                                                                                                                                                                                        Wild-type multiple tumour suppressor (MTS) gene and mutant sequences - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma
                                                                                                                            Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6.6; DB 1; Length 16; Pred. No. 7e+02; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 12; Page 68; 156pp; English.
                                                                                                                                                                                                                                                                          94US-00214581.
94US-00214582.
94US-00215088.
94US-00227369.
94US-00251938.
                                  AAQ99935 standard; DNA; 16 BP.
                                                                                                        Human MTS1 RT-PCR primer, X2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.6%;
                                                                                                                                                                                                                                                    95WO-US003316
                                                                                                                                                                                                                                                                                                                                                   (MYRI-) MYRIAD GENETICS INC
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 69.2
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-344401/44.
                                                                                                                                                                                                                                                                                                  18-MAR-1994;
14-APR-1994;
01-JUN-1994;
                                                                                                                                                                                                      WO9525429-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             or leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cherapeutics
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                    17-MAR-1995;
                                                                                                                                                                                                                                                                          18-MAR-1994;
18-MAR-1994;
                                                                                  07-MAY-1996
                                                                                                                                                                                                                              28-SEP-1995
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                                                           AAQ9935;
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            RESULT 666
                        4AQ99935,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer; polymerase chain reaction; PCR; amplification; P16; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - also DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting polymorphism associated with cancer presdisposition - also DNN vectors and host cells e.g. for gene or protein replacement therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                              Multiple tumour suppressor; MTS1; cancer; diagnosis; assay; predisposition; melanoma; leukaemia; lymphoma; prognosis; pancreas; breast; thyroid; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6.6; DB 1; Length 16; Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Multiple tumour suppressor 1 gene PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Kamb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; Page 68; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Cannon-Albright LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT69788 standard; DNA; 16 BP.
                                                                                                                                                                                                                                          94US-00214582.
94US-00215086.
94US-00215087.
94US-00227369.
94US-00251938..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.6%;
                                                                                                                                                                                                           95WO-US003537
                                                                                                                                                                                                                                                                                                                                                     FOUND
                                                                                                                                                                                                                                                                                                                                                   (UTAH ) UNIV UTAH RES FOUND (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.27
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 ctrccrégacace 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P16 promoter primer X2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-344626/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                               18-MAR-1994;
14-APR-1994;
01-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                        Skolnick MH,
                                                                                                                                       W09525813-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5624819-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-1997.
                                                                                                                                                                                                           17-MAR-1995;
                                                                                                                                                                                                                                            18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
10-SEP-1997
                                                                                                                                                                         28-SEP-1995.
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                                                                                                       Synthetic.
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AAT00727 standard; DNA; 16 BP.

AAT00727

RESULT 667
AAT00727/C
ID AAT007
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AC AAT007

CTACGTGTACAGG 19

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CTTCCTGGACACG

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Primers AAV11256 and AAV11257 are used in the isolation of the human multiple tumour suppression proteins, MTS1 and MTS1E1-beta. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are useful for the diagnosis of cancers related to MTS1E1-beta mutation(s) and their
                   This is the nucleotide sequence of a PCR primer used for amplification in
                             the method of the invention involving the used of the multiple tumour suppressor (MTS) gene, to diagnose and treat cancer. The MTS gene is nucleful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies to replace the expression constructs can also be used for recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for function in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTS1; WTS2; multiple tumour suppressor; diagnosis; cancer;
germ-line mutation; familial melanoma locus; MLM; predisposition; ss.
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                              23.6%; Score 6.6; DB 1; Length 16; 69.2%; Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                           Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human MTS1 and MTS1E1-beta PCR primer X2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 12; Col 81-82; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00214582.
94US-00215086.
94US-00215087.
94US-00227369.
94US-00251938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV11257 standard; DNA; 16 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00487033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 69.27
Best Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                     7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                         13 crrccrccacacaca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-250421/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5739027-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV11257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 670
AAV11257/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids based on multiple tumour suppressor, MTS, sequences - useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS mutation(s).
                                                                                                                                                                                                                                                                     Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                  The present sequence is primer for the PCR amplification of the P16 promoter. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multiple tumour suppressor; MTS; human; cancer; hybridisation; somatic mutation; gene therapy; PCR; primer; amplification; so
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6.6; DB 1; Length 16;
Pred. No. 7e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                 Skolnick MH;
                                                                                                                                                                                                                                                                                                                            Example 12; Col 81-82; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mucleotide sequence of PCR primer 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 12; Col 51; 73pp; English
         94US-00214582.
94US-00215086.
94US-00215087.
94US-00227369.
94US-00257369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV53838 standard; DNA; 16 BP.
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94US-00215086.
94US-00215087.
94US-00227369.
94US-00251938.
                                                                                                                                                                                             Cannon-Albright LA, Kamb A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00480810
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                                                                                                                                          GENETICS INC
                                                                                                                                                            UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 69.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCCTGGACACG 1
                                                                                                                                                                                                                                   WPI; 1997-258217/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-494842/42
                                                                                                                                        (MYRI-) MYRIAD
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01-JUN-1994;
17-MAR-1995;
                                                               14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-1994;
           18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5801236-A
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18-MAR-1994;
                                                   8-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV53838;
                                                                                                                                                              (UTAH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kamb A;
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Best Loca Matches

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RESULT 671

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The invention relates to the isolation of the gene encoding the human multiple tumour suppressor 1 (MTS1) (AAA9563). The MTS1 protein has a vertostatic activity and is used in protein replacement therapy. This sequence is a PCR primer used in the amplification of the beta-specific form of the P16 promoter. MTS1 is useful in diagnosing human cancers such as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma, cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of pancras, breast, stomach, brain, prostate, bladder, thyroid, ovary, uterus, testis, kidney, colon and rectum. The MTS1 gene and protein is useful in gene therapy, protein replacement therapy and protein mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTS; human; polymorphism detection; cancer predisposition; astrocytoma;
Multiple Tumour Suppressor gene; melanoma; leukaemia; glioblastoma;
lymphoma; glioma; Hodgkin's lymphoma; chronic lymphocytic leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protein composition useful in protein replacement therapy for diagnosing and treating cancer comprises a specific weight percent of human multiple tumor suppressor 1 polypeptide.
                                                                                       Cytostatic, human, multiple tumour suppressor 2; MTS2; diagnostic; cancer; gene therapy; protein replacement therapy; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.6%; Score 6.6; DB 1; Length 16; Best Local Similarity 69.2%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer for human MTS1Elbeta coding sequence.
                                                    Human P16 promoter beta-specific primer X2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; Col 49; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ48793 standard; cDNA; 16 BP
                                                                                                                                                                                                                                                                                                                              94US-00215086.
94US-00215087.
94US-00227369.
94US-00251938.
                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US003316.95US-00480810.
                                                                                                                                                                                                                                                                       97US-00986515
                                                                                                                                                                                                                                                                                                           94US-00214582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CTACGTGTACAGG 19
                  14-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 CTTCCTGGACACG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-514036/46.
                                                                                                                                                                                                                                                                                                                                                                      14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000
                                                                                                                                                                                                                                                                       08-DEC-1997;
                                                                                                                                                                                            US6090578-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                                             18-MAR-1994
                                                                                                                                                                                                                                                                                                                                  18-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kamb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 67
  $$$$$$$$$$$$$$$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primers AAV70600-02 were used to amplify a human multiple tumour suppressor 2 (WTS2) gene. The MTS2 gene unclectide sequence can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glacoma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys. (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse multiple tumour suppressor gene segment - useful for primer design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; multiple tumour suppressor 2 gene; MTS2; cancer; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                        Gaps
lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum
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                                                                                              23.6%; Score 6.6; DB 1; Length 16; 69.2%; Pred. No. 7e+02; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer X2B for multiple tumour suppressor 2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                          Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 14; Col 54; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA95654 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                 AAV70602 standard; DNA; 16 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US003316.
95US-00487033.
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                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
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Best Local Similarity 69.2.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 CTACGTGTACAGG 19
                                                                                                                                                                             7 CTACGTGTACAGG 19
                                                                                                                                        9; Conservative
                                                                                                                                                                                                                   13 crrccresión 1
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                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2003
03-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5843756-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                    Query Match
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Gaps

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AAA95654/c ID AAA956 XX AC AAA956 RESULT 672

Mon Apr 19 15:55:12 2004

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Human P16 PCR primer SEQ ID NO:23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA39372 standard; DNA; 16 BP.
                                                                                                                                                  94US-00215086.
94US-00215087.
94US-00227369.
94US-00251938.
95WO-US003316.
                                                                                    95US-00486047
                                                                                                                              94US-00214582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 crrccreeacace 1
                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-038259/03
                                                                                                                                                  18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
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                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1998;
    US5994095-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6060301-A.
                                              30-NOV-1999
                                                                                                                              18-MAR-1994
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                                                                                                                                                                                                                                                                                                                  Kamb A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is a PCR primer for DNA encoding human WTSIElbeta. The invention relates to a method for diagnosing a polymorphism associated with a predisposition to cancer by detecting a germ-line alteration of a wild-type Multiple Tumour Suppressor (MTS) gene or its expression products in a human sample. The method comprises detecting a germ-line alteration of a wild-type MTS gene or its expression products in a human sample. The method comprises detecting a germ-line alteration of a wild-type MTS gene or its expression products in a human sample, the alteration indicating a predisposition to at least one of the cancers. The cancer is selected from melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodckin's lymphoma, chronic lymphocytic leukaemia (CLL), and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The method may be used as the basis for developing very important diagnostic tests capable of basis for developing very important diagnostic tests capable of progression of multiple tumour types and may provide means for a general anti-cancer therapy by virtue of its ability to suppress tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multiple tumour suppressor; MTS2; human; diagnosis; Hodgkin's lymphoma; cancer predisposition; melanoma; leukaemia; lymphoma; glioma; MTS1; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing a polymorphism associated with a predisposition for cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer for human multiple tumour suppressor 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.6%; Score 6.6; DB 1; Length 16; 69.2%; Pred. No. 7e+02; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Skolnick MH, Cannon-Albright LA, Kamb A;
therapy; MTS1Elbeta; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 12; Col 48; 74pp; English.
                                                                                                                                                                                                     94US-00214582.
94US-00215086.
94US-00215087.
94US-00227369.
95WO-US003537.
95US-00474083.
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                                                                                                                                                                    97US-00848251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTCCTGGACACG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                          Homo sapiens.
                                                                                                                                                                 29-APR-1997;
                                                                                                                                                                                                                                                                                       01-JUN-1994;
17-MAR-1995;
07-JUN-1995;
                                                                               USS989815-A
                                                                                                                       23-NOV-1999
                                                                                                                                                                                                                             18-MAR-1994
18-MAR-1994
                                                                                                                                                                                                                                                                        14-APR-1994
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Homo sapiens

Synthetic

RESULT

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This sequence represents a PCR primer for the human multiple tumour suppressor 1 (MTS1) coding sequence. The invention relates to the human MTS2 DNA and protein sequences. The DNA sequences are useful for diagnosing or determining a prediction to cancers e.g. melanoma, leukaemia, lymphoma, glioma, Hodgkin's lymphoma and cancers of the pancreas, breast, thyroid, ovary, kidney, uterus and stomach
Multiple tumor suppressor cDNA, useful for diagnosing or determining a predisposition to cancer.
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; multiple tumour suppressor; MTS; somatic mutation; cancer; diagnosis; germ line mutation; gene therapy; cytostatic; melanoma; leukaemia; astrocytoma; glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; PCR primer; ss.
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                                                                                                                                                                                                                            23.6%; Score 6.6; DB 1; Length 16; 69.2%; Pred. No. 7e+02;
                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                 0; Mismatches
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94US-00215086.
94US-0027369.
94US-00251938.
95WO-US003316.
95US-00480810.
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17-MAR-1995;
07-JUN-1995;
08-DEC-1997;
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WPI; 2000-269915/23

Kamb A;

(MYRI-) MYRIAD GENETICS INC

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                                                                                                                                                                        The present invention describes a vector (I) comprising an isolated DNA sequence of a multiple turnour suppressor (MTS) gene having a sequence of a multiple turnour suppressor (MTS) gene having a polymucleotide sequence of the human MTSIEL-beta. (I) is useful for introducing wild-type MTS function to a cancerous or pre-cancerous cell introducing wild-type MTS function to a cancerous or pre-cancerous cell which carries diminished or mutant MTS alleles for suppressing neoplastic growth of the recipient cells. (I) is also useful for increasing the level of expressed at a normal level but the gene product is not fully gene is expressed at a normal level but the gene product is not fully contional. A host cell transformed with (I) is useful as a model system to study cancer remission and drug treatment which promotes such remission. The present invention relates to somatic mutations and germ prognosis of human cancer e.g. melanoma, leukaemia, astrocycom, glioblastoma, lymphoma, glioma, Hodskin's lymphoma, and cancers of the panch in the present invention relates, testis, kidney, stomach and rectum. The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                            New vector useful for gene therapy of cancer associated with mutation in tumor suppressor gene, comprises DNA sequence of multiple tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variant; human; multiple tumour suppressor; MTS; mutation; melanoma; cancer; diagnosis; PCR primer; ss.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human multiple tumour suppressor 1 primer X2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 23.6%; Score 6.6; DB 1; Local Similarity 69.2%; Pred. No. 7e+02; Nes 9; Conservative 0; Mismatches
                                                                                                                                                    Example 12; Col 48; 71pp; English.
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94US-00215086.
94US-00215087.
94US-00227369.
95WO-US003316.
95US-00480810.
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                                                                   WPI; 2000-349676/30.
                                                                                                                          suppressor gene.
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07-JUN-1995;
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14-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA11186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                          Kamb A;
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                                                                                                   The invention relates to variants (AAA11196-A11206) of the human multiple tumour suppressor 1 (MTS1) gene (AAA11165). The variants have the following changes relative to this sequence: A at any of positions 265, 442, 330 and 329; T at any of positions 172, 238, 341 and 148 and deletions of nucleotides 290-294, 172-179 or 128-129. The variants are somatic mutations of MST1, indicative of predisposition to melanona and many other cancers, so detecting them is useful for diagnosis, prognosis and monitoring of cancer (including prenatal analysis). Cells and animals that express the variants are useful as model systems for identifying potential anticancer agents. This sequence represents a primer used to screen for MTS1 Elbeta initial mRNA expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human multiple tumor suppressor-2 (MTS2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel multiple tumor suppressor gene useful for diagnosing, prognosing and treating cancers, such as melanoma, leukemia, glioblastoma and
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
New mutants of the human multiple tumor suppressor gene, useful as diagnostic markers of cancer, contain specific base alterations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; multiple tumour suppressor; MTS; cancer; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                             Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; Col 48; 71pp; English.
                                                                          Example 12; Col 48; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00214582.
94US-00215086.
94US-00215087.
94US-00251938.
95WO-US003316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00486047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF58190 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 crrccresacace 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-158668/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6180776-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MUT-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF58190;
                                        deletions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kamb A;
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99WO-US013820

17-JUN-1999;

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New multiple tumor suppressor 2-specific antibodies useful for detecting differences in the absence of the peptides or mutant gene products, or for screening tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to an antibody or its fragment that specifically binds to a human multiple tumour suppressor (MTS). The invention is useful for detecting differences in the absence of MTS peptides, to screen a tissue or to detect mutant MTS gene products. The antibodies will immunoprecipitate MTS proteins from solution as well as react with MTS protein on Western or immunoblots of polyacrylamide gels
                                                                            MTS; Multiple Tumour Suppressor; cancer; antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; Col 48; 71pp; English.
                                                  Primer X2B used in the invention.
                                                                                                                                                                                                        94US-00214582.
94US-00215086.
94US-00215087.
94US-00227369.
95WO-US003316.
95US-00486047.
                                                                                                                                                                                 98US-00120128
                                                                                                                                                                                                                                                                                                                  (MYRI-) MYRIAD GENETICS INC
                         23-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-014867/02.
                                                                                                                                                                                                                                                14-APR-1994;
01-JUN-1994;
17-MAR-1995;
07-JUN-1995;
                                                                                                     Homo sapiens
                                                                                                                                                                                 22-JUL-1998;
                                                                                                                               US6140473-A.
                                                                                                                                                                                                           18-MAR-1994;
18-MAR-1994;
                                                                                                                                                       31-OCT-2000
                                                                                                                                                                                                                                       18-MAR-1994
 AAC83090;
                                                                                                                                                                                                                                                                                                                                             Kamb A;
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98US - 0089844P 98US - 0089828P 98US - 0089992P 98US - 0089993P 98US - 0089993P 98US - 0089993P 98US - 00899997P 98US - 00899997P 98US - 0090003P 98US - 0090003P 98US - 0090041P 98US - 0090041P 98US - 0090044P 98US - 0090044P

19 - CUN - 1998; 19 - CUN - 1998;

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                                                      0; Gaps
Query Match 23.6%; Score 6.6; DB 1; Length 16; Best Local Similarity 69.2%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 4; Indels
                                                                                                          7 CTACGTGTACAGG 19
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New polynucleotide useful in cancer immunotherapy.

Roberts BL, Shankara S;

WPI; 2000-106132/09.

(GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.

Claim 1; Page 54; 97pp; English.

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SAGE tag; serial analysis of gene expression; diagnosis; differential gene expression; characterisation; targetted expression; tumour; cancer; immunotherapy; ss.
                                                                                                                             Human breast tumour downregulated gene SAGE tag, SEQ ID NO:49.
                                                          AAZ79758 standard; DNA; 10 BP
                                                                                                         10-APR-2000 (first entry)
                                                                                  AAZ79758;
                                  RESULT 681
                                                 AAZ79758
                                                            BXBXBXEXEXBXBXBXBXBXBXB
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Homo sapiens WO9966303-A2.

23-DEC-1999

Sequences AAZ79710-279916 represent SAGE (serial analysis of gene expression) tags used to identify mana transcripts which are carpered in a variety of normal or malignant cell types. Gifferentially expressed in a variety of normal or malignant cell types. Some of the transcripts correspond to known genes or ESTS (expressed composition) and the particular cell type, while other differentially expressed in that particular cell type, while other transcripts correspond to novel genes. The invention also provides a transcripts correspond to novel genes. The invention also provides a nucleotide comprising a promoter sequence derived from one of the differentially expressed genes, which may optionally be operably linked to a foreign nucleotide sequence, and gene delivery vehicles and host comprising the polynucleotides of the invention. A nucleotide comprising the polynucleotides of the invention. A nucleotide comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures to characterise a cell of a specific tissue type and to determine whether it is normal or malignant. They may be used to screen for agents that computer/foreign gene construct of the invention may be used for targetted expression of differentially expressed genes compound. The promoter derived from a gene preferentially expressed in derafitic cells (antigen-presenting cells, or APCS), may be operably confirmed to a sequence encoding an immune tresponse by educating immune effector cells in vivo, or in cancer immunotherapy 22.9%; Score 6.4; DB 1; Length 10; 87.5%; Pred. No. 5.4e+02; Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other; Best Local Similarity Query Match 

gene. The invention is useful for diagnosing, prognosing and treating cancers. It is also useful for screening drugs for cancer therapy and

13 CTTCCTGGACACG 1

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14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                     US6218146-B1
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                                                                                                   04-JUL-2001
                                                                                                                                                                                                                                                           17-APR-2001.
                                                                                                                                                                                                                                                                                                                18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995
                                                                             AAD04711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Kamb A;
                                Matches
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents PCR primer X2B used in analysis of multiple trumour suppressor MTS1 and MTS2. The MTS genes, and expression products, are useful for treating, diagnosing or prognosing human cancer. In particular, the MTS gene is useful for diagnosing a predisposition to or as a gene therapy for melanoma, leukaemia, astrocytoma, gliobastoma, prophema, chronic lymphatic leukaemia (CLL), prymphoma, glioma, gliobastoma, chronic lymphatic leukaemia (CLL), or cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach or rectum. The gene may be used in both cancerous and pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mouse multiple tumor suppressor gene, useful for diagnosing or prognosing human cancer or as gene therapy for treating cancer, particularly melanoma, leukemia, astrocytoma, lymphoma or cancers of the pancreas or breast.
                                                                                                                                                                                                                                                                        Human; multiple tumour suppressor; MTS1; MTS2; therapeutic; diagnostic; carcer; gene therapy; melanoma; leukaemia; astrocytoma; glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; chronic lymphatic leukaemia; PCR primer; ss.
                                                                                                                                                                                                                                                         PCR primer X2B used in analysis of multiple tumour suppressor MTS1/2.
                                                                                         Gaps
                                                                                        ;
0
                                                               Query Match
23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                            Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Col 51; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US003316.
95US-00487033.
95US-00508735.
                                                                                                                                                                                         AAS02583 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                        98US-00201139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stone S, Jiang P, Kamb A;
                                                                                                                                                                                                                                   29-AUG-2001 (first entry)
                                                                                                            7 CTACGIGIACAGG 19
                                                                                                                               crrccregacace 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-280859/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -cancerous cells
                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1995;
07-JUN-1995;
28-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                           US6210949-B1.
                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1998;
                         gene therapy
                                                                                                                                                                                                                                                                                                                                                                                  03-APR-2001
                                                                                                                                                                                                              AAS02583;
                                                                                                                                                                  RESULT 678
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                                                                                                                                                                                                                                                                                                                           GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel multiple tumor suppressor proteins useful for diagnosis and prognosis of human cancer and for screening drugs for cancer treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                            Human; multiple tumour suppressor; MTSIElbeta; cytostatic; germ line mutation; gene therapy; melanoma; leukaemia; astrocytoma; glioblastoma; lymphoma; gliobma; Hodgkin's lymphoma; cancer; rectum; panoreas; breast; thyroid; ovary; uterus; testis; kidney; stomach; somatic mutation; MTS; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                       Human MTS and MTS1Elbeta sequence amplifying primer, X2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Col 52; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC83090 standard; DNA; 16 BP.
AAD04711 standard; DNA; 16 BP.
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94US-00215087.
94US-00227369.
94US-00251938.
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                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                crrccreakcace 1
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AAC83090/c
ID AAC830
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Gaps

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4; Indels

DB 1; Length 16;

Query Match
23.6%; Score 6.6; DB 1;
Best Local Similarity 69.2%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches

7 CTACGIGIACAGG 19

Matches

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; ichthyosis; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BSI) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; skin; dermatological; vulnerary; antipporiatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                          Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGB; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 6.4; DB 1; Length 11;
Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Hofmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 24; Page 268; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV63172 standard; cDNA; 11 BP.
                                                                                                                                                                                                                                                                                       20-DEC-2001; 2001WO-EP015179.
                                                                                                                                                                                                                                                                                                                              03-JAN-2001; 2001DE-01000127.
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87.5%;
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5°
                                                                                                                                                                                                                                                                                                                                                                                                             Conradt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GGAGTCCA 26
                                                                                                                                                                                                                                                                                                                                                                   (HENK ) HENKEL KGAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-590638/63.
                                       Human skin EST 8379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. skin cancer.
                                                                                                                                                                                                     WO200253774-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             Petersohn D,
  21-OCT-2002
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-2002
                                                                                                                                                                                                                                             11-JUL-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis in to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sumburn, psoriasis; scleroderma; inchthyosis; atopic dermatitis, acne, seborrhea; lupus erythematosus; rosacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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                                                                                                                                                                                                                                                                                                                                                Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, 8s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
    Gaps
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    Indels
    7
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Pred. No. 6e+02;
0; Mismatches
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 179; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petersohn D, Conradt M, Hofmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV70593 standard; cDNA; 11 BP.
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                                                                                                                                                                                    ABV67783 standard; cDNA; 11 BP.
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ilarity 87.5%;
Conservative
                                                                                                                                                                                                                                                                     (first entry)
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skin. The present seque
(EST) of the invention
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                                                                                                                                                                                                                                                                                                          Human skin EST 5569
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Best Local Similarity
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RESULT 68: ABV70593/c ID ABV7( XX AC ABV7(

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Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
                                      Petersohn D, Conradt M, Hofmann K;
                                                                                   Disclosure; Page 51; 1345pp; German.
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    20-DEC-2001; 2001WO-EP015179.
                03-JAN-2001; 2001DE-01000127.
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                                                                        e.g. skin cancer.
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Hofmann K;

Conradt M,

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis, acne; seborrhea; lupus erythematosus;
                                                                                  The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma, ichthyosis, atopic dermatitis, acne, sebornhea; lupus erythematosus; rosacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BST) of the invention
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                                                  Claim 24; Page 275; 1345pp; German.
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e.g. skin cancer.
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BP

ABI10705 standard; DNA; 12

RESULT 688

ABI10705,

(first entry)

22-FEB-2002

ABI10705;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABR00010-ABF9989, ABH0010-ABH9989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic former from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 273568 for detecting SNP TSC0003234.
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22.9%; Score 6.4; DB 1; Length 11;
Best Local Similarity 87.5%; Pred. No. 6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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                                                                                 Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                         SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                            Oligonucleotide primer SEQ ID NO 310678 for detecting SNP TSC0024049.
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Best Local Similarity 87.5-
Local 7; Conservative
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Query Match 22.9%; Score 6.4; DB 1; Length 12; Best Local Similarity 87.5%; Pred. No. 6.5e+02; Matches 7; Conservative 0; Mismatches 1; Indels

8 TACGIGTA 15 TACGCGTA 10

ò 쉽 (EPIG-) EPIGENOMICS AG.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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peptide nucleic acid, cytosine methylation; cardiovascular, primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
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                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 22.9%; Score 6.4; DB 1; Length 13; Best Local Similarity 87.5%; Pred. No. 6.8e+02; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 49822; 29pp + Sequence Listing; German.
                                                                                                                                                                           Claim 1; SEQ ID NO 49821; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 13 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                              was obtained in electronic format from Wl
ftp.wipo.int/pub/published_pct_sequences
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                                  X,
                                  Berlin
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                                  Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TACGIGTA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methylation status.
                                                                   WPI; 2001-657177/75.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disponsis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABR0010-ABH99999 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide SEQ ID NO 37742 for detecting SNP TSC0011735.
                                                                                                                                                                                                                                                                                                 22.9%; Score 6.4; DB 1; Length 13; 87.5%; Pred. No. 6.8e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 37742; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13 BP; 3 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Sequence 13 BP; 4 A; 4 C; 2 G; 2 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was obtained in electronic format from Wi
ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          8 TACGTGTA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                   11 TACGCGTA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2001
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ABC37725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 37741; 29pp + Sequence Listing; German.
       Length 13;
                                                                         1; Indels
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Score 6.4; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                       RESULT 693
ABC37724/C
D
XX
ABC37724;
XX
ABC37724;
XX
ABC37724;
XX
C
D1gonuclectide SEQ ID NO 37741 9
XX
SNP; single nuclectide polymorph:
XX
XX
Homo sapiens.
XX
XX
Homo sapiens.
XX
XX
YX
C6-APR-2001; 2001W0-IB000713.
XX
XX
XX
YA
C6-APR-2001; 2001W0-IB000713.
XX
XX
XX
C18-C12001.
XX
XX
XX
C1-APR-2001; 2001W0-IB000713.
XX
XX
XX
C1-APR-2001; 2001W0-IB000713.
XX
XX
C1-APR-2001; 2001W0-IB000713.
XX
XX
XX
C1-APR-2001; 2001W0-IB000713.
XX
C1-APR-2001; 2001W0-IB00000-ABF999999, ABCCC
C1-APR-2001W0-IB00010-ABF99999, ABCCC
C1-APR-2001W1-APR-209999, ABCCCC
C1-APR-2001W1-APR-20909, ABCCCCC
C1-APR-2001W1-APR-20909, ABCCCCC
C1-APR-2001W1-APR-20909, ABCCCCC
C1-APR-2001W1-APR-20909, ABCCCCC
C1-APR-2001W1-APR-2001W1-APR-20909, ABCCCCC
C1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-2001W1-APR-
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   22.9%;
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                                                                         Conservative
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       Query Match
Best Local Similarity
Matches 7; Conserv
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ADB00353/c
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is canceded at chromosome 7022.1. MD24 is encoded at chromosome 6921.3-22.2. MD27 is encoded at chromosome 6921.3-22.2. MD27 is encoded at chromosome 6921.3-22.2. MD27 is encoded at chromosome 16911.2 and MD212 is encoded at chromosome 16921.3-22.2. MD27 is manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23 mD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are protein are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
                                                                                                                             Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                           duman MDZ3 scanning oligonucleotide SEQ ID 1339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; SEQ ID NO 1339; 103pp; English.
                                                                                                                                                                                                                                                                                                                                        30-JUL-2002; 2002EP-00016874
                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2001; 2001US-00922181
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shannon M, Gu Y, Nguyen C;
                                                    20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-423107/40.
                                                                                                                                                                                                                                                                                                                                                                                                                 (AEOM-) AEOMICA INC
                                                                                                                                                                                                                            Homo sapiens
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                  ADB00353;
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Matches
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                                22.9%; Score 6.4; DB 1; Length 17; 62.5%; Pred. No. 7.4e+02; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; immunostimulant; gene therapy; vaccine; human;
Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                    Human MDZ3 scanning oligonucleotide SEQ ID 1340.
                                                                                                                                                                                                                                                           ADB00354 standard; DNA; 17 BP
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                                                                                                                  7 CTACGTGTACAGGGAG
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                      Local Similarity 62.
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chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 7q22.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                 New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                    present invention relates to novel human zinc finger-containing
                                                                                                                                                                                                                                                  Example 8; SEQ ID NO 1340; 103pp; English.
                                                                                                    30-JUL-2002; 2002EP-00016874
                                                                                                                       02-AUG-2001; 2001US-00922181
                                                                                                                                                           Shannon M, Gu Y, Nguyen C;
                                                                                                                                         (AEOM-) AEOMICA INC.
                                                                                                                                                                              WPI; 2003-423107/40.
                                            Homo sapiens,
                                                              EP1281758-A2
                                                                                 05-FEB-2003
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proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 1g21.3-22.2, MD27 is encoded at chromosome 1g21.3-22.2, MD27 is encoded at chromosome 1g22.3.2 is encoded at chromosome 1g22.3 is encoded at chromosom

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                                                                Query Match 22.9%; Score 6.4; DB 1; Length 17; Best Local Similarity 62.5%; Pred. No. 7.4e+02; Matches 10; Conservative 0; Mismatches 6; Indels
Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
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Gaps
                                                                                               Human MDZ3 scanning oligonucleotide SEQ ID 1342.
                                                         ADB00356 standard; DNA; 17 BP
             7 CTACGTGTACAGGGAG 22
                        16 crcgcrcccccacarac 1
                                                                                  (first entry)
                                                                                  20-NOV-2003
                                                                      ADB00356;
                                             RESULT 696
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Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.

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EP1281758-A2

05-FEB-2003

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30-JUL-2002; 2002EP-00016874.
                                                                                                                                                                             02-AUG-2001; 2001US-00922181.
                         WPI; 2003-423107/40.
                                                                                                                                                                                  (AEOM-) AEOMICA INC
               (AEOM-) AEOMICA INC
                                                                                                                                                              EP1281758-A2.
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                   05-FEB-2003
                                                                                                                             ADB00357;
                                                                                                                   RESULT 697
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ3 is canceded at chromosome 7422.1, MDZ4 is encoded at chromosome 7422.1, MDZ4 is encoded at chromosome 6921.3-222.2, MDZ7 is encoded at chromosome 6921.3-222.2, MDZ7 is encoded at chromosome 1691.2 and MDZ12 is encoded at chromosome corin manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MD21; MD21; MD21; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                     New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.9%; Score 6.4; DB 1; Length 17; 62.5%; Pred. No. 7.4e+02; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                          Example 8; SEQ ID NO 1343; 103pp; English.
                                                                                                                                                                                      MDZ4, MDZ7 or MDZ12, e.g. cancer.
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Shannon M, Gu Y, Nguyen C;
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Matches 10; Conservative
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                                                 WPI; 2003-423107/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ4, MDZ4, MDZ12. MDZ3 is encoded at chromosome 7422.1, MDZ4 is encoded at chromosome 7422.1, MDZ7 is encoded at chromosome 6P21.3-22.2, MDZ7 is encoded at chromosome 16P1.2 and MDZ12 or increating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ1, or MDZ12, or MDZ12, or MDZ12, or MDZ12, or MDZ12. The nucleic acused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acused in MDZ3, MDZ4, MDZ7, or MDZ12. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                     New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
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                                                 30-JUL-2002; 2002EP-00016874.
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                                                                                                     02-AUG-2001; 2001US-00922181
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Gaps ., New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ1 or MDZ12, e.g. cancer.

WPI; 2003-423107/40.

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD212, MD23. MD23 is encoded at chromosome 7422.1, MD24 is encoded at chromosome 6721.3-22.2, MD27 is encoded at chromosome 6721.3-22.2, MD27 is encoded at chromosome 6721.2 and MD212 is encoded at chromosome 1671.2 and MD212 sequences are useful in therapy, or immunifacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease acids and proteins are also useful for diagnosing or monitoring a disease acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch 22.9%; Score 6.4; DB 1; Length 25; 1 Similarity 62.5%; Pred. No. 5.9e+02; 10; Conservative 0; Mismatches 6; Indels
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Cytostatic, immunostimulant, gene therapy; vaccine; human, zinc finger protein; MD23; MD24; MD212; chromosome 7g22.1; czncomcome 6p21.3-22.2; chromosome 16p11.2; chromosome 15g26.1; cancer; developmental disorder; ss. Human MDZ3 scanning oligonucleotide SEQ ID 2836. 30-JUL-2002; 2002EP-00016874 02-AUG-2001; 2001US-00922181 (AEOM-) AEOMICA INC. EP1281758-A2, 05-FEB-2003 

Gu Y, Nguyen C; Shannon M,

WPI; 2003-423107/40.

New zinc finger-containing proteins and nucleic acids, useful in manifacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

WPI; 2001-657177/75.

Claim 1; SEQ ID NO 300881; 29pp + Sequence Listing; German.

Example 8; SEQ ID NO 2836; 103pp; English.

The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 15p11.2 and MDZ12 is encoded in therapy, 15p11.2 and MDZ12 sequences are useful in therapy,

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or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for disgnosing or monitoring a disease caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 72.7
Matches 8; Conservative
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        ABI21821;
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                                                                                                                                                                                                                                                                                                      SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                     Gaps
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Query Match 22.1%; Score 6.2; DB 1; Length 12; Best Local Similarity 72.7%; Pred. No. 7e+02; Matches 8; Conservative 0; Mismatches 3; Indels
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                                                             7 CTACGTGTACA 17
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ABI21821 ID ABI2

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 321794 for detecting SNP TSC0030495.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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Best Local Similarity 72.7
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                        Claim 1; SEQ ID NO 337428; 29pp + Sequence Listing; German.
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nes 8; Conservative
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DB 1; Length 12; 3; Indels

22.1%; Score 6.2; DB 1; 72.7%; Pred. No. 7e+02; tive 0; Mismatches

Berlin K;

ABI22910 standard; DNA; 12

12 TGTATATGTAG

22-FEB-2002 (first entry)

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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pot_sequences
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Best Local Similarity 72.7%; Pred. No. 7e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tapeseen the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 322883 for detecting SNP TSC0031094.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABF82073 tepseent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleot acid; cytosine methylarion; cardiovascular; primer; as: central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF0010-ABF99999, ABH0010-ABF99999 and ABT00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. .. 0 Oligonucleotide SEQ ID NO 90253 for detecting SNP TSC0022616. Claim 1; SEQ ID NO 118026; 29pp + Sequence Listing; German. 22.1%; Score 6.2; DB 1; Length 13; 72.7%; Pred. No. 7.3e+02; cive 0; Mismatches 3; Indels Claim 1; SEQ ID NO 90253; 29pp + Sequence Listing; German. Seguence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequences Berlin K; 멾 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. 07-APR-2000; 2000DE-01019173 ABC90236 standard; DNA; 13 (first entry) Query Match
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                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABF99899, ABR0010-ABF99899, ABR0010-ABF99989 and ABI00010-ABF92073 represent the oligoners described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                               Score 6.2; DB 1; Length 13; Pred. No. 7.3e+02; 0; Mismatches 3; Indels
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                                                                                Oligonucleotide SEQ ID NO 160516 for detecting SNP TSC0040412.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Matches 8; Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cancer also vased for addiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                         oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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GTAAACGTAGT 12

(first entry)

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75

Claim 1; SEQ ID NO 182915; 29pp + Sequence Listing; German.

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABF
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                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 160514 for detecting SNP TSC0040412.
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                 07-APR-2000; 2000DE-01019173
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                                                                                                                                                                                                        Local Similarity 72.7
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                                         Olek A, Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                   Claim 1; SEQ ID NO 160515; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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AAF46048 standard; DNA; 15

RESULT 724

(first entry)

30-MAR-2001

AAF46048;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but the oligomers cancer from the remaining form the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                           Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
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22.1%; Score 6.2; DB 1;
Best Local Similarity 72.7%; Pred. No. 7.3e+02;
Matches 8; Conservative 0; Mismatches 3;
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligomorelectie, (for Insulin-like Growth Factor [108]) in the seeptor, IGF binding protein [IGFBB] - or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomuclectide which can be used to design the antisense oligomuclectide which can be used to design the antisense oligomuclectides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, inhiposis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, nooplasias, scleroderma, warts, benign growths, cancers of the skin, a hypernevacular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, hyperproliferation of the inside of blood
                                                                                                                                                            Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic, cytostatic, dermatological, cardiant; virucide, ophthalmological, keloid, skin disorder, Insulin-Ilke Growth Factor. I receptor; IGF-1; pityriasis; IGF binding protein, IGFB-2; IGFBP3; inflammation, psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborincea; ruba; kearcosis; neoplasia; solaroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neobascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
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                                                                                                                            IGFBP2 oligonucleotide #887.
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RESULT 725

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12 TGTACAGGGAG 22

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Query Match

Best Loc Matches

TGTATATGTAG 2

12

IGFBP2 oligonucleotide #885.

(first entry)

30-MAR-2001

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The present invention relates to a method for ameliorating the effects of antisense oligonucleotide, (for Insulan-like Growth Factor [107] receptor, 107 binding protein [107] Landing the skin with an receptor, 107 binding protein [107] Landing growth factor mediated cell proliferation, inhibiting or reducing growth factor mediated cell proliferation, and lammation and/or other disorders of present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153 oligonucleotides of the present invention (see AAF45151 and AAF45153 ichthyosis, pityriasis, ruba, pilaris, serborrhoez, keloids, keratosis, ineoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic
                                                                                                                                                     Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin disorder, Insulin-like Growth Factor. I receptor; IGF-1, pityriasis, IGF binding protein, IGFBP-2, IGFBP3, inflammation, psoriasis, pityriasis, growth factor mediated cell proliferation, ichthyosis, serborrhoea, ruba, keatosis, neoplasia, scleroderma, wart, skin cancer, sclerotic disease, hyperneovascular condition, hyperplasia, kidney disease, neovascular condition, hyperplasia, kidney disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
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  AAF46045 standard; DNA; 15 BP
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                                                                                                                   GFBP2 oligonucleotide #884.
                                                                            (first entry)
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AAF46046 standard; DNA; 15 BP AAF46046 RESULT 726 AAF46046 ID AAF460 XX AC AAF460

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Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin disorder, insulin-like Growth Factor. I receptor; IGF-1, pitryriasis, IGF binding protein, IGFBP-2, IGFBP3, inflammation, psoriasis, plaris; growth factor mediated cell proliferation, ichthyosis, serborrhoea, ruba, keratosis, neoplasia, scleroderma, wart, skin cancer; sclerotic disease, hyperneovascular condition, hyperplasia, kidney disease, neovascular condition, hyperplasia, kidney disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0140345P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Werther GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-041421/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200078341-A1.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wraight CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-2000
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligomuclectide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBB3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomuclectide which can be used to design the antisense oligomuclectides of the present invention (see AAF45151 and AAF45153-6150muclectides of the present invention (see AAF45151 and AAF45153-6150muclectides of the present invention see AAF45151 and AAF45153-6160thyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, incoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood Example 6; Page 39; 201pp; English.

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                               Gaps
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22.1%; Score 6.2; DB 1; Length 15; 72.7%; Pred. No. 7.7e+02; tive 0; Mismatches 3; Indels
                            Conservative
                                                        7 CTACGTGTACA 17
            Local Similarity
hes 8; Conserv
Query Match
                            Матсрев
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Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

vessels or any other hyperplasia

ВP AAF46047 standard; DNA; 15 (first entry) 4 crcccrcckch 14 30-MAR-2001 CXXXXXXXXX 요

IGFBP2 oligonucleotide #886

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Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic, cytostatic, dermatological; cardiant; virucide, ophthalmological; keloid; skin disorder, Insulin-Ilke Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBB3; inflammation; psoriasis; pitaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keartosis; neoplasia; sclaroderma; wart; skin cancer; sclarotic disease; hyperneovascular condition; hyperlasia, kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for ameliorating the effects of skin disorders. The method comparises contacting the skin with an antisense oligomucleotide, (for Insulan-like Growth Factor [IGF] receptor, IGF binding protein [IGFBP] or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present esquence is an oligomucleotide which can be used to design the antisense oligomucleotides of the present invention (see AAF45151 and AAF45153 oligomucleotides of the present invention (see AAF45151 and AAF45153 inchthyosis, pityriasis, ruba, plants, serborthoea, keloids, keratosis, inchthyosis, pityriasis, ruba, plants, serborthoea, keloids, keratosis, hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic condition, which we have a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic condition of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 39; 201pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-1999; 99US-0140345P.
                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2000; 2000WO-AU000693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wraight CJ, . Werther GA,
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                                                                                                                                                                                                                                                                    WO200078341-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation.
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Gaps
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Query Match
22.1%; Score 6.2; DB 1; Length 15;
Best Local Similarity 72.7%; Pred. No. 7.7e+02;
Matches 8; Conservative 0; Mismatches 3; Indels
                     Best Loca
Matches
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7 CTACGTGTACA 17 3 crecerdeach 13 g

AAT54219 standard; RNA; 15 (revised)
(first entry) 25-MAR-2003 24-MAR-1997 AAT54219; RESULT 728 AAT54219/ %%%%#X#X%%

ВБ.

Human IL-5 hammerhead ribozyme target sequence (nt. position 91)

Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor;

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TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; (ML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; hommation; arthritis; psoritasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                     94US-00201109.
94US-00218934.
94US-00222495.
94US-00227958.
94US-00228041.
94US-0028041.
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94US-00291433.
94US-00292620.
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94US-00300000.
94US-00303039.
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94US-00345516
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94US-00314397
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                                                                         Homo sapiens.
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02-SEP-1994;
08-SEP-1994;
                                                                                                                                                                                                                                                             23-SEP-1994;
28-SEP-1994;
03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
04-NOV-1994;
                                                                                       W09523225-A2
                                                                                                                                                                                                      15-AUG-1994;
16-AUG-1994;
                                                                                                                                                                                                                                                     23-SEP-1994;
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18-MAY-1994;
                                                                                                                                                                                                                      17-AUG-1994;
                                                                                                                                                                                                                                                                                                                                             30-JAN-1995;
                                                                                                        31-AUG-1995
                                                                                                                                                                                              06-JUL-1994;
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(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD; Tracz D, Usman N, Wincott FE, Woolf T;

WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.

Claim 2; Page 214; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-5) mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistence. The ribozymes cleave the IL-5 target sequences and thereby inhibit IL-5 expression, making them useful for treating chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes and preventing the recruitment and activation of eosinophils. The ribozymes can also be used to treat eosinophilia (related to parasitic infection or with pulmonary infiltration) and L-tryptophan-associated eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI

ВЪ

ADB00350 standard; DNA; 17

ADB003

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(first entry)

20-NOV-2003

ADB00350;

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ3 is cancoded at chromosome 7422.1, MDZ4 is encoded at chromosome 6721.3-22.2, MDZ7 is encoded at chromosome 6721.2 and MDZ12 is encoded at chromosome 1671.2 and MDZ12 is encoded at chromosome 1522.2.2, MDZ7, and MDZ12 is encoded at chromosome 1671.2 and MDZ12 is encoded at chromosome 1522, and MDZ12 is encoded at chromosome 1522, and a discalar associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids and proteins are also not MDZ13, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross at the attention microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7g22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15g26.1; cancer; developmental disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                        Gaps
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                                                                Length 15;
                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
                  Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MDZ3 scanning oligonucleotide SEQ ID 1335.
                                                            Query Match

22.1%; Score 6.2; DB 1;
Best Local Similarity 72.7%; Pred. No. 7.7e+02;
Matches 8; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; SEQ ID NO 1335; 103pp; English.
                                                                                                                                                                                                                                                                                                      ADB00349 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gu Y, Nguyen C;
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                                                                                                                                               14 TACAGGGAGTC 24
                                                                                                                                                                                           14 TACACGTAGGC 4
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ADB00349/c
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ3 is cocoded at chromosome 7422.1, MDZ4 is encoded at Chromosome 6721.3-22.2, MDZ7 is encoded at chromosome 6721.2, and MDZ12 is encoded at chromosome 5921.3-22.2, MDZ7 is encoded at chromosome 1671.2 and MDZ12 is encoded at chromosome 502.0 in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross also be used as probes to detect and characterize gross cades and also be used as probes to detect and characterize gross alterations in MDZ3, MDZ7, or MDZ12 genetic locus. The probes are proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
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                                                                                                                                                                                                                                                              Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ4; MDZ4; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                                                        Human MDZ3 scanning oligonucleotide SEQ ID 1336.
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ID ADB00352 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                      developmental disorder; ss
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Page 322

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ12. MDZ3 is proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ12. MDZ3 is encoded at chromosome 7422.1, MDZ4 is encoded at chromosome 6PZ1.3 = 22.2., MDZ7 is encoded at chromosome 16P11.2 and MDZ12 is encoded at chromosome 16P11.2 and MDZ12 is encoded at chromosome 16P12 in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; SEQ ID NO 1337; 103pp; English.
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ID ADB00348 standard; DNA; 17 BP.
                                                                                                                                                                                                                                30-JUL-2002; 2002EP-00016874.
                                                                                                                                                                                                                                                                               02-AUG-2001; 2001US-00922181
                                                                                                                                                                                                                                                                                                                                                                             Shannon M, Gu Y, Nguyen C;
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Best Local Similarity 72...
8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 TGCACACGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-423107/40.
                                                                                                                                                                                                                                                                                                                                (AEOM-) AEOMICA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                      Homo sapiens
                                                                                                                                    EP1281758-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-2003
                                                                                                                                                                                 05-FEB-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BXXXXXXXXXXXXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ4, MDZ4, MDZ12. MDZ3 is encoded at chromosome 6P21.3-22.2, mDZ7 is encoded at chromosome 6P21.3-22.2, MDZ7 is encoded at chromosome 6P21.3-22.2, MDZ7 is encoded at chromosome 16P1.2 and MDZ12 is encoded at chromosome 16P1.2 and MDZ12 is encoded at chromosome 16P1.3-22.2, MDZ7 is encoded at chromosome 16P1.2 and MDZ12 is encoded at chromosome 16P1.3-22.2, MDZ7 is encoded at chromosome 16P1.3-22.2, MDZ7 is encoded at chromosome 16P1.3-22.2, MDZ7 is encoded at chromosome 16P1.3-22.2, MDZ7, MDZ7, or MDZ12, encoder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acused by altered expression of MDZ3, MDZ7, or MDZ12. The nucleic acide can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                    Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; immunostimulant, gene therapy; vaccine; human;
zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7g22.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.1%; Score 6.2; DB 1; Length 17; 72.7%; Pred. No. 7.6e+02; Antive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MDZ3 scanning oligonucleotide SEQ ID 1337.
                                                                                                             Human MDZ3 scanning oligonucleotide SEQ ID 1338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; SEQ ID NO 1338; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2002; 2002EP-00016874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001; 2001US-00922181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gu Y, Nguyen C;
                                                              20-NOV-2003 (first entry)
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es 8; Conserv
                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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Matches

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Gaps ö

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.

Example 1; Page 62; 81pp; English

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Zinc finger protein related oligonucleotide target SEQ ID NO:2453.
                                                                                                                                                                                                                                                                                                                                              Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                              (SANG-) SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2000; 2000US-00716637.
                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2001; 2001WO-US043438
                                                                                                                                                                                                                                                                                             ABQ72155 standard; DNA; 9 BP
     30-JUL-2002; 2002EP-00016874.
                  02-AUG-2001; 2001US-00922181
                                        Shannon M, Gu Y, Nguyen C;
                                                                                                                                                                                                                                                                                                                      28-AUG-2002 (first entry)
                                                                                                                                                                                                                                                    12 TGTACAGGGAG 22
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                                                    WPI; 2003-423107/40.
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                             (AEOM-) AEOMICA INC
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2002
                                                                                                                                                                                                                                                                                                         ABQ72155;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu Q;
                                                                                                                                                                                                                                                                                RESULT 734
ABQ72155
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ12. MDZ3 is encoded at chromosome 7g22.1, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 6p21.3-22.2, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ2, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ4 is encoded at chr
New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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22.1%; Score 6.2; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; SEQ ID NO 1334; 103pp; English.
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (P2), and a third (F3) cand a third (F3), and a third (F3), and a third (F3) target site, condrises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (II); (2) a polymucleotide (III) encoding (I) or (III); and (S1) designing (II) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S3 target subsite, and selecting the F2 zinc finger such that it binds to the S3 target subsite, and selecting the F2 zinc finger such that it binds to the S3 target subsite, and selecting of triplet target subsites at target site. (I) is useful for recognition of triplet target subsites are useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject. In modulate the expression of a target region of target mucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their carget sequences, as well as enhanced biological activity, ABQ71213 to ABG72214 and ABBF8191 to ABBF1230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present

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Gaps
                                                                                                                                                                  Zinc finger protein related oligonucleotide target SEQ ID NO:2454.
                                   ö
                                                                                                                                                                                     Zinc finger protein; ZFP; DNA binding protein; zinc finger; 88
                                   0; Indels
                Query Match
21.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels
Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                ABQ72156 standard; DNA; 9 BP.
                                                                                                                                                    28-AUG-2002 (first entry)
                                                    2 GGGCCC 7
                                                                     3 GGGCCC 8
                                                                                                                                   ABQ72156;
                                                                                                 RESULT 735
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New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.

(SANG-) SANGAMO BIOSCIENCES INC. 20-NOV-2000; 2000US-00716637. 20-NOV-2001; 2001WO-US043438.

WO200242459-A2 Homo sapiens. Synthetic.

30-MAY-2002.

WPI; 2002-500284/53.

Liu O;

; 0

Gaps ö

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WPI; 2003-567233/53.
                                                        Query Match
Best Local Similarity
                                                                                                           JS2003068675-A1.
                                                                                                                                     (ring/) rin o
                                                                                                               10-APR-2003
                                                                                                       Synthetic.
                                                                                   ADA64482;
                                                                                                                                         Liu O;
                                                                          RESULT 736
                                                          Best Loc
Matches
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Designing zinc finger protein that has three zinc fingers from N-terminus and C-terminus that bind to subsites in 3' to 5' direction, in a target site, by selecting zinc fingers that bind their respective subsites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of designing a zinc finger protein. The method is useful for designing a zinc finger protein. The method provides multi-finger zinc finger proteins with improved affinity and specificity for their target sequences, as well as enhanced biological activity. The present sequence represents a zinc finger protein DNA target sequence.
                                                                                                                     The invention relates to a method of designing a zinc finger protein. The method is useful for designing a zinc finger protein. The method provides multi-finger zinc finger proteins with improved affinity and specificity for their target sequences, as well as enhanced biological activity. The present sequence represents a zinc finger protein DNA target sequence.
and C-terminus that bind to subsites in 3' to 5' direction, in a target site, by selecting zinc fingers that bind their respective subsites.
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.4%; Score 6; DB 1; Length 9; 100.0%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                       DB 1; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; target sequence; zinc finger protein; multi-finger zinc finger protein; improved affinity; improved specificity; enhanced biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                          Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                       21.4%; Score 6; DB 1
100.0%; Pred. No. 1.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc finger target sequence DNA #941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27; 34pp; English.
                                                                             Disclosure; Page 27; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAR-1999; 99US-0126238F.
24-MAR-1999; 99US-0126239F.
30-ULL-1999; 99US-014655SF.
23-MAR-2009; 2000US-00535008.
20-NOV-2000; 2000US-00516637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA64483 standard; DNA; 9 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2001; 2001US-00990186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 6, Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGGCCC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFXEXCCCCCXS
                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                  The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) cainc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (II); (2) a polymucleotide (III) encoding (I) or (III); and (S3) designing (II); (1) a polymucleotide (III) encoding (I) or (III); and (S3) designing (IV); (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F2 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites a target site. (I) is useful for recognition of triple target subsites are modulate the expression of a target region within a subject, in modulate the expression of a target region within a subject, in modulate the expression of a target region within a subject, in a sample, and in assays to determined the phenotype and function of an a sample, and in assays to determined the phenotype and function of the present carget sequences, as well as enhanced biological activity. AB071213 to the finger peptides which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Designing zinc finger protein that has three zinc fingers from N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.4%; Score 6; DB 1; Length 9; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; target sequence; zinc finger protein; multi-finger zinc finger protein; improved affinity; improved specificity; enhanced biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc finger target sequence DNA #940.
                               Example 1; Page 62; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAR-1999; 99US-0126238P.
24-MAR-1999; 99US-0126339P.
30-ULL-1999; 99US-0146595P.
23-WAR-2000; 2000US-00535008.
20-NOV-2000; 2000US-00516637.
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Mismatches		
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Matches	<b>λ</b> δ	qq

Search completed: April 19, 2004, 15:00:31 Job time: 4 secs

140

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

April 19, 2004, 15:45:29; Search time 0.001 Seconds (without alignments) 202.496 Million cell updates/sec Run on:

US-10-024-396-3-COPY 28 Title: Perfect score: Sequence:

1 cgggccctacgtgtacagggagtccagg 28

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

422 Total number of hits satisfying chosen parameters:

211 segs, 3616 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 213 summaries

Pending-NA, Main \*:qpwd Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description Sequence US-09-922-181A-2836 US-09-922-181A-2844 US-09-954-427A-1081B7 US-09-954-427A-134734 US-09-956-584-2663 US-10-714-195-197 US-08-983-605-203 US-09-532-263-19 SUMMARIES Length Query Result 8

equence 1337, equence 1338, equence 1338, equence 1338, equence 134, equence 5, h, equence 135, equence 105, equence 1	equence 1633 equence 1633 equence 1633 equence 1633 equence 231, pequence 231, pequence 2159, equence 2159, equence 1331, equence 23131, equence 24833 equence 6950, equen	ι ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο	equence 33, 7 equence 3490 equence 3760 equence 1766 equence 1766 equence 2951 equence 2951 equence 2950 equence 4147
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US-10-305-274-1406
US-10-367-832A-33165
US-10-367-832A-33165
US-10-367-832A-33165
US-10-367-832A-34829
PCT-US02-25940-14568
PCT-US02-25943-51163
PCT-US02-25943-51163
US-09-406-643-897
US-09-406-643-897
US-09-406-643-897
US-09-912-673A-55
US-09-912-673A-55
US-10-27-565-14568
US-10-37-68-3163
US-10-387-787-25557
US-10-367-832A-51163
US-10-367-832A-31163
US-10-367-832A-31163
US-10-367-832A-31163
US-10-367-832A-31163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
PCT-US02-19183-20/c
PCT-US040ENC 20, Application PC/TUS0239183
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGCCCTACGTGTACAGGG 20
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Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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5, Appli
41393, A
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                  US-10-471-271-2304-
US-10-471-271-2305-
US-10-623-107-2950-
US-10-623-107-2950-
US-10-623-107-2950-
US-10-623-107-2950-
US-10-623-107-2950-
US-10-623-107-2950-
US-10-623-107-2950-
US-10-339-764-2305-
US-10-339-764-2305-
US-10-305-275-941-
US-09-274-5336-143-
US-09-274-5536-143-
US-09-274-5538-143-
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US-10-227-565-41393
US-10-367-882A-41393
US-10-310-128-34441
PCT-US03-10296-20
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PCT-US01-18815-7
PCT-US01-26488-60
PCT-US01-26488-60
PCT-US01-26488-60
PCT-US02-25940-18950
PCT-US02-25942-4864
PCT-US02-25943-22682
PCT-US02-25943-3161
PCT-US02-25943-14828
PCT-US02-25943-48484
PCT-US02-25943-62741
US-10-277-565-18850
US-10-227-565-18850
US-10-227-565-18828
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US-10-367-892-18950
US-10-362-25943-33165
PCT-USO2-25943-33165
PCT-USO2-25943-34829
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-10-367-729A-6581
-10-367-832A-22682
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US-10-367-832A-37161
US-10-367-832A-48484
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JS-10-227-567-6581
JS-10-287-787-27958
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Sequence 22105, A Sequence 6183, Ap Sequence 31163, A Sequence 31163, A Sequence 12401, A Sequence 1856, A Sequence 897, App

6183, Ap 31163, Ap 31163, Ap 897, App 21, App 21, App 73, App 73, App 73, App 73, App 7162, App 1163, Ap 1163, Ap 1163, Ap 22163, Ap 22163, Ap 22163, Ap

Sequence Sequence Sequence

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Gaps RESULT 1
PCT-USO2-39183-19/C
Sequence 19 Application PC/TUSO239183
Sequence 19 Application PC/TUSO239183
SEGUENT INFORMATION:
APPLICANT: NEOMETH W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
FILE REPERRICE: RISP-0453
CURRENT APPLICATION NUMBER: PCT/USO2/39183
CURRENT APPLICATION NUMBER: 10/024,396
PRIOR PILING DATE: 2001-12-09
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 91
LENGTH: 20 ö Length 20; Indels ; Score 20; DB 1; Pred. No. 4.2; 0; Mismatches

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Query Match
Best Local Similarity 84.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches
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llarity 84.0%; Pred. No. 13;
Conservative 0; Mismatches
              Mismatches
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; Sequence 2839, Application US/09922181A
; GENERAL INFORMATION:
                                                          9 ACGTGTACAGGGAGTCCAGG 28
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2841
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                       RESULT 5
US-09-922-181A-2841
              20;
              Matches
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APPLICANT: Kenneth W. Dobie
APPLICANT: Isis Pharmaceuticals, Inc.
TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
FILE REPERENCE: RTSP-0453
CURRENT APPLICATION NUMBER: PCT/US02/39183
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 10/024,396
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 91
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/10024396
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF CD3611 EXPRESSION
FILE REFERENCE: RTS-0339
CURRENT APPLICATION NUMBER: US/10/024,396
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 91
LENGTH: 20
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US-10-024.396-20/c

US-10-024.396-20/c

Sequence 20, Application US/10024396

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TILLE OF INVENTION: ANYISENSE MODULATION OF CD36L1 EXPRESSION

TILLE REPERENCE: RTS-0339

CURRENT APPLICATION NUMBER: US/10/024,396

CURRENT FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 91

LENGTH: 20
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                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
TOTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-39183-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonucleotide US-10-024-396-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-396-19
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-024-396-19/c
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RESULT 6
US-09-922-181A-2842
; Sequence 2844, Application US/09922181A
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
APPLICANT: NGUVEN: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ4, MDZ7 AND
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND
FILE REFERENCE: AEOMICA-12
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SEQ ID NO 2842
; SEQ ID NO 2842
; LENGTH: 25
                                                                                                                                                                                                      Sequence 2841, Application US/09922181A
| Sequence 2841, Application US/09922181A
| Separation: APPLICANT: Gu, Yizhong
| APPLICANT: Bhannon, Mark
| APPLICANT: Bhannon, Mark
| APPLICANT: Bhannon, Mark
| APPLICANT: Brand | APPLICANT: Brand | APPLICANT: MOVEN, Cung-fuong
| TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ4, MDZ7 AN | FILE REPRENCE: AEOMICA-12
| TITLE OF INVENTION: DATE: 1001-12-12
| NUMBER OF SEQ ID NOS: 7046
| SOFTWARE: AFOMICA Sequence Listing Engine | SEQ ID NO 2841
| LENGTH: 25
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APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: SUGNEY, CUNG-TWONG
TITLE OF INVENTION: FOUR HYMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 ANI
FILE REFERENCE: AEOMICA-12
CURRENT APPLICATION NUMBER: US/09/922,181A
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Gaps
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Sequence 2818, Application US/09922181A
Sequence 2818, Application US/09922181A
GENERAL INFORMATION:
APPLICANT: Shanon, Mark
APPLICANT: Shanon, Mark
APPLICANT: Shanon, Mark
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ4, MDZ7 ANI
FILE REFERENCE: AEOMICA-12
CURRENT APPLICATION NUMBER: US/09/922,181A
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SEQ ID NOS: 7046
SEQ ID NO 2938
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GENERAL INFORMATION:
APPLICANT: Mittman, Michael
ITITE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
FILE REFERENCE: 3115.1
CURRENT APPLICATION NUMBER: US/09/956,584
CURRENT APPLICATION NUMBER: 00/234,017
PRIOR PILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 312298
LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Mittmann, M
APPLICANT: Mittmann, M
TITLE OF INVENTION: methods of Genetic Analysis of Mus
TITLE OF INVENTION: musculus
FILE REPREBRENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT PILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 318766
LENGTH: 25
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Pred. No. 18
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Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Mus musculus
US-09-956-584-315298
                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA; CRGANISM: Homo sapiens
US-09-922-181A-2838
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US-60-234-017-318766
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US-09-956-584-315298
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Sequence Listing Engine
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: NGU/GA, CUNG-TUONG
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND
TITLE OF INVENTION: POUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ7 AND
TITLE OF SEQ ID NOS: 7046
SOUTHWARE: ADOIL 12-12
NUMBER OF SEQ ID NOS: 7046
SEQ ID NO 2837
ILENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2840, Application US/09922181A

Sequence 2840, Application US/09922181A

GENERAL INFORMATION:

APPLICANT: Gu, Vizhong

APPLICANT: Ghannon, Mark

APPLICANT: Gunnon, Mark

APPLICANT: Gunnon, Mark

APPLICANT: Wouven, Cung-Thong

TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND

FILE REFERENCE: AEOMICA-12

CURRENT FILING DATE: 2001-12-12

NUMBER OF SEQ ID NOS: 7046

SOFTWARE: Aeomica Sequence Listing Engine

SEQ ID NO 2840

LENGTH: 25
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Best Local Similarity 87.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches
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Best Local Similarity 87.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2839
LENGTH: 25
TYPE: DN Aeomica Sequence Listing Engine
TYPE: USA
CORGANISM: Aeomica Sequence Listing Engine
SEQ ID NO 2839
US-09-922-181A-2839
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CORGANISM: Homo sapiens
US-09-922-181A-2837
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US-09-922-181A-2840
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Best Local Similarity
Matches 19; Conserv
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Sequence 2836, Application US/09922181A
Sequence 2836, Application US/09922181A
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
APPLICANT: Nauyen, Cung-Thong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7
FILE REFERENCE: AEOMICA-12
CURRENT APPLICATION NUMBER: US/09/922,181A
CURRENT APPLICATION NUMBER: US/09/922,181A
NUMBER OF SEQ ID MOST: 2001-12-12
SOFTWARE: Aeomica Sequence Listing Engine
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US-60-427-808-248399
is-60-427-808-248399, Application US/60427808
j GENERAL INFORMATION:
j APPLICANT: Xue Mei Zhou
i ITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
l TILE OF INVENTION: Methods of Genetic Analysis of Mouse;
j CURRENT FILING DATE: 2002-11-20
i NUMBER OF SEQ ID NOS: 982914
j SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
j SEQ ID NO 248399
j LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 25;
                  APPLICANT: Xue Mei Zhou
ITILE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 248399
LENGTH: 25
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90.0%; Pred. No. 26;
tive 0; Mismatches
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61.4%; Score 17.2; I
Best Local Similarity 86.4%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches
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Best Local Similarity 90.0
Matches 18; Conservative
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ORGANISM: Homo sapiens
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CORGANISM: Mus musculus
US-60-427-808-248399
                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-248399
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Best Local Similarity
Matches 19; Conserv
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LENGTH: 25
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APPLICANT: Shannon, Mark
APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ4, MDZ7 AND
TITLE OF INVENTION: POUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ4, MDZ7 AND
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SSQ ID NO 2843
ILBNGTH: 25
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GENERAL INFORMATION

APPLICANT: Michael Mittmann

TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome

FILE REPERENCE: 3112.1

CURRENT APPLICATION NUMBER: US/09/954,427A

CURRENT FILING DATE: 2001-09-17

FRIOR PELING DATE: 2000-09-18

NUMBER OF SEQ ID NOS: 420907

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Pred. No. 19;
0; Mismatches
                                                                                                                 Query Match 63.6%; Score 17.8; Dest Local Similarity 90.5%; Pred. No. 18; Matches 19; Conservative 0; Mismatches
               ) PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: Genbank AW123720

US-60-234-017-318766
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US-10-719-900-248399
; Sequence 248399, Application US/10719900
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Best Local Similarity 83.3%;
Matches 20; Conservative
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CRGANISM: Rattus Norvegicus
US-09-954-427A-59195
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; ORGANISM: Homo sapiens
US-09-922-181A-2843
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US-09-954-427A-59195
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US-09-922-181A-2843
ORGANISM: Mus
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Gaps
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TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REPERENCE: 3121
CURRENT APPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 22855
LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Mitchael
TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus FILE REFERENCE: 3115.1
CURRENT APPLICATION NUMBER: US/09/956,584
CURRENT PILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,017
PRIOR FILING DATE: 2000-09-20
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
ERO ID NO 2663
LENGTH: 25
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 134734
LENGTH: 25
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                                                                                                                                                                                  Score 16.6; DB
Pred. No. 28;
0; Mismatches
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                                                                                                                                                                                  Query Match
Best Local Similarity 82.6%;
Matches 19; Conservative
                                                                                             ; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-134734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-2663
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Best Local Similarity
Matches 19; Conserv
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US-10-355-577-592056/c
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GENERAL INFORMATION:
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: Nguyen, Cung-Thong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
CURRENT APPLICANTS: US/09/922,181A
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SSQ ID NO 2844
LENGTH: 25
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TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
FIRE REPERENCE: 3112.1
CURRENT APPLICATION WHERE: US/09/954,427A
CURRENT FILING DATE: 2001-09-17
FIRE PAPLICATION NUMBER: 60/233,166
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 420907
SEQ ID NO 108187
LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome FILE REFERENCE: 3112.1
CURRENT APPLICATION NUMBER: US/09/954,427A
CURRENT APPLICATION NUMBER: 60/233,166
PRIOR APPLICATION NUMBER: 60/233,166
PRIOR FILING DATE: 2000-09-18
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Pred. No. 28
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GENERAL INFORMATION:
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Best Local Similarity 82.6%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.6'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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US-09-954-427A-108187/c
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TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REPERBNCE: 3121
CURRENT PAPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2.002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
EBNGTH: 25
Sequence 592056, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Mittenan, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT PAPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Mcroarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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APPLICANT: Affymetrix, inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: musculus
FILE REFERENCE: 3115
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31888
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.3%; Score 16.6; I 82.6%; Pred. No. 28; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 59.3%; Score 16.6; I
82.6%; Pred. No. 28;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AV359510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.6;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-60-234-017-31888
; Sequence 31888, Application US/60234017
; GENERAL INFORMATION:
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; Sequence 23855, Application US/60353987
; GENERAL INFORMATION:
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82.6%;
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.6
Matches 19; Conservative
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; ORGANISM: Homo sapien
US-60-353-987-23855
                                                                                                                                                                                                                                                     TYPE: DNA
) ORGANISM: Homo sapien
US-10-355-577-592056
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Best Local Similarity
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Matches
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US-05-922-181A-1336

Sequence 1336. Application US/09922181A
Sequence 1336. Application US/09922181A
Septence 1336. Application:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: FOUR HUMAN
TITLE OF INVENTION: FOUR HUMAN
CURRENT APPLICANTION WUMBER: US/09/922,181A
CURRENT APPLICATION TOWNER: 2001-12-12
URRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: Cung-Tuong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 ANI
FILE REFERENCE: AECMICA-12
CURRENT APPLICATION NUMBER: Us/09/922,181A
CURRENT APPLICATION NUMBER: Us/09/922,181A
NUMBER OF SEQ ID NOS: 7046
SEQ ID NO 1335
LENGTH: 17
TYPE: DNA
TYPE: DNA
TYPE: DNA
TYPE: DNA
OKGANIEM: Homo sapiens
US-09-922-181A-1335
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TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILLE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
ERGTH: 25
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Indels
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59.3%; Score 16.6; I
Best Local Similarity, 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.4%; Score 14.4; 93.8%; Pred. No. 25
                                                                                                                                                                                         ; Sequence 592056, Application US/60353987; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1335, Application US/09922181A; GENERAL INFORMATION:
                                                                    3 CCCACGTGTACAGGGGGTTCCGG 25
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19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-592056
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hes 15; Conserv
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US-60-353-987-592056/c
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Best Local S
Matches 15
Matches
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4 GCCCTACGTGTACAGGGAG 22
                ) OTHER INFORMATION: primer US-10-713-457-197
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US-10-714-195-197/c
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       FEATURE:
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FORGUMEN 1977-197/C

GENERAL 1977, APPLICATION

GENERAL 1977, APPLICATION:

APPLICANT: Genomic Health

APPLICANT: Gal, Hebron University Hostipal

APPLICANT: Stak, Offre

APPLICANT: Stak, Steve

APPLICANT: Stak, Steve

TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR

TITLE OF INVENTION: POSITIVE CANCER

TITLE OF INVENTION: POSITIVE CANCER

TITLE OF INVENTION NUMBER: PCT/US03/36777

CURRENT APPLICATION NUMBER: PCT/US03/36777

CURRENT APPLICATION NUMBER: 60/427090

PRIOR FILING DATE: 2003-11-15

NUMBER OF SEQ ID NOS: 372

SOFTWARE FELING DATE: 2003-11-15

LENGTH: 20

LENGTH: 20

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LENGTH: 20
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baker, Joffree
APPLICANT: Cronin, Maureen
APPLICANT: Baselga, Jose
ITILE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
ITILE OF INVENTION: POSITIVE CANCER;
ITILE OF INVENTION: OSSITIVE CANCER;
ITILE OF INVENTION: AND THE 2003-11-13
CURRENT FILING DATE: 2003-11-13
FRIOR APPLICATION NUMBER: 60/427090
FRIOR FILING DATE: 2003-11-15
NUMBER OF SEQ ID NOS: 372
SOFTWARE FASTESEQ FOR Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.4%; Score 14.4; D
Best Local Similarity 93.8%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches
                                                                                                                                                       Query Match 51.4%; Score 14.4; D
Best Local Similarity 93.8%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1336
LENGTH: 17
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                               3 GGCCCTACGTGTACAG 18
                                                                                                                                                                                                                                                                                1 GGCCTACGTGCAG 16
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                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-181A-1336
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LENGTH: 20
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Sequence 203, Application US/08983605A

Sequence 203, Application US/08983605A

Sequence 203, Application US/08983605A

SETERAL INFORMATION:

TITLE OF INVENTION: Microsatellite Markers for Plants of the Species

TITLE OF INVENTION: Triticum Aestivum and Tribe Triticase and the Use of

TITLE OF INVENTION: Said Markers

TITLE OF INVENTION: Said Markers

TITLE OF INVENTION: Said Markers

CURRENT APPLICATION NUMBER: US/08/983,605A

CURRENT FILING DATE: 1998-05-01

SERLIER PRING DATE: 1995-06-28

NUMBER OF SEQ ID NOS: 466

SEQ ID NO 203

LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.4%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 37;
     Length 20;
                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                             APPLICANT: BACK, Joffre
APPLICANT: Groin, Maureen
APPLICANT: Shak, Steve
APPLICANT: Shak, Steve
APPLICANT: BACH, Steve
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
TITLE OF INVENTION: POSITIVE CANCER
FILE REFERENCE: 39740-0005
CURRENT APPLICATION NUMBER: US/10/714,195
CURRENT PILING DATE: 2003-11-14
FRIOR APPLICATION NUMBER: 60/427090
FRIOR FILING DATE: 2003-11-15
NUMBER OF SEQ ID NOS: 372
SOFTWARE: FactSEQ for Windows Version 4.0
LENGTH: 20
Query Match
51.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                    Sequence 197, Application US/10714195 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                        6 CCTACGTGTACAGGGA 21
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CRGANISM: Triticum aestivum
US-08-983-605-203
                                                                                                                                                             20 CCIACGGGTACAGGGA
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Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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// OTHER INFORMATION: primer US-10-714-195-197
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Sequence 1338, Application US/09922181A
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AN
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                             CURRENT APPLICATION DATE:

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/853,105
FILING DATE: 10-May-2001
CLASSIFICATION NUMBER: US/09/853,105
FILING DATE: 10-May-2001
CLASSIFICATION NUMBER: US/08/702,665
FILING DATE: 20-DEC-1996
ATTORNEY/ABOT INFORMATION:

NAME: PRESENT LEOPOID
REFERENCE/DOCKET NUMBER: 10296
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFOR
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88.2%; Pred. No. 31;
cive 0; Mismatches
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84.2%; Pred. No. 45;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 CGTGTACAGGGAGTCCAGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ccreractresastresas 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GCCCTACGTGTACAGGG 20
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.7
Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 36
US-09-922-181A-1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-922-181A-1337
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                                                                                                                                      RESULT 33
US-09-532-563-19
Sequence 19, Application US/09532263
Sequence 19, Application US/09532263
Sequence 19, Application US/09532263
TITLE OF INVENTION: A NOVEL HARMOPOLETIN RECEPTOR NUMBER OF SEQUENCES 25
CORRESPONDENCE ADDRESS: CORT, MURPHY & PRESSER STREET 400 Garden City Plaza
CITY: Garden City
STREET: New York
COUNTER: New York
COUNTER: New York
COUNTER: New York
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/532,263
FILING DATE: 22-APT-2000
CLASSIFICATION: CURROWN-
PRIOR APPLICATION: CURROWN-
PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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GENERAL INFORMATION:
PAPLICANT Hilton, Douglas J.
TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 400 Garden City Plaza
CITY: Garden City
STREET: We York
CUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.7%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REPERENCE/DOCKET NUMBER: 10296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
TELEPA: (516) 742-4366
TELER: 203 901 SANS UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 CGTGTACAGGGAGTCCAGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 21 base pairs
19 GCCTTAGGCGTACAGGGAG 1
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STRANDEDNESS: single
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Sequence 1334, Application US/09922181A
Sequence 1334, Application US/09922181A
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: NGUYEN, CUNG-TUONG
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AN
FILE REPERENCE: ADOMICA-12
CURRENT APPLICATION NUMBER: US/09/922,181A
CURRENT FILING DATE: 2001-112-12
NUMBER OF SEQ ID NOS: 7046
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1334
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:

A METHOD FOR ENHANCING NEURONE

TITLE OF INVENTION:

A METHOD FOR ENHANCING NEURONE

CORRESPONDERS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREE: 400 Garden City Plaza

CITY: Garden City Plaza

CITY: Garden City Plaza

CITY: 10.8.A.

ZITP: 11530

COMPUTRY: U.S.A.

ZITP: TOWN YOR

COMPUTRY: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Perentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,792

FILING DATE: 10-CUL-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: 31,346

RESIFICATION NUMBER: 31,346

REPERRENCE/DOCKET NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 31,346
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TELEFAX: 230 901 SANS UR
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base palrs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.4;
Pred. No. 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08633792
GENERAL INFORMATION:
1 CIACGIGIGCAGCGAGT 17
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TELEFAX: (516)742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGCCCTACGTGTACA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 decerracerereca 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-922-181A-1334
                                                                       RESULT 39
US-09-922-181A-1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-633-792-6/c
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APPLICANT: GL, Yizhong
APPLICANT: GL, Yizhong
APPLICANT: Glamnon, Mark
APPLICANT: Shannon, Mark
TITLE CANT: Nquyen, Cung-Tuong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ4, MDZ7 AND
FILE REFERENCE: AEOMICA-12
CURRENT APPLICATION WUMBER: US/09/922,181A
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1340
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1339, Application US/09922181A
GENERAL INFORMATION:
APPLICANT: Gu, Yizhon
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND
FILE REPERBNCE: AEOMICA-12
CURRENT APPLICATION NUMBER: US/09/922,181A
CURRENT FILIAG DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SOFTWARE: Aeomica Sequence Listing Engine
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Best Local Similarity 88.2%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 31; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                 Query Match

49.3%; Score 13.8;
Best Local Similarity 88.2%; Pred. No. 31
Matches 15; Conservative 0; Mismatche
                      CURRENT APPLICATION NUMBER: US/09/922,181A
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SETWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1338
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1340, Application US/09922181A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 CCTACGTGTACAGGGAG 22
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     FILE REFERENCE: AEOMICA-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-181A-1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1339
                                                                                                                                                                                TYPE: DNA
GORGANISM: Homo sapiens
US-09-922-181A-1338
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US-09-922-181A-1339
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LENGTH: 17
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              Query Match
Best Local Similarity 93.3%; Pred. No. 42;
Matches 14, Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

47.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 42
US-09-918-779-15/c
; Sequence 35, Application US/09918779
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
                                             17 reracadedadreca 3
US-08-633-792-6
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TYPE: DNA
CRGNISM: Artificial Sequence
FRATURE:
CHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
CTHER INFORMATION: primers
US-09-918-779-35
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.3%; Pred. No. 54;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
US-10-624-932-35/c
i Sequence 35, Application US/10624932
i GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 TACAGGGAGTCCAGG 28
Spaderna, Steven
Shimkets, Richard
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 TAGAGGGAGTCCAGG 3
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Sequence 49862. Application US/10310188

GENERAL INFORMATION:
APPLICANT: ROSELEGEMONICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES 147497
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT APPLICATION 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SSO ID NO 49862
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/10159856
Sequence 39, Application US/10159856
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPIRITE REPERBNCE: RTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 39
LENGTH: 20
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87.1%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
47.1%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                       Indels
                                                                                                                                         Score 13.2; DB 1;
Pred. No. 45;
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ORGANISM: Artificial Sequence
FEATURE:
TOTHER INFORMATION: Antisense Oligonucleotide
US-10-159-856-39
                                                                                                                                                                             Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-159-856-105; Sequence 105, Application US/10159856; GENERAL INFORMATION:
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                                                                                                                                         47.1%;
illarity 83.3%;
Conservative
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US-10-310-188-49862
                          TYPE: DNA
CONGANISM: Homo sapiens
US-10-310-188-57779
                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
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US-10-310-188-49862
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US-10-159-856-39/c
LENGIH: 18
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Seguence 57779, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSettademonics
ATTLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REPRENDENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER: OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 57779
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FRICK APPLICATION NUMBER: 05/918,779
FRICK APPLICATION NUMBER: 05/21,409
FRICK APPLICATION NUMBER: 05/221,409
FRICK APPLICATION NUMBER: 05/222,840
FRICK APPLICATION NUMBER: 05/222,840
FRICK APPLICATION NUMBER: 05/222,840
FRICK APPLICATION NUMBER: 05/223,752
FRICK APPLICATION NUMBER: 05/223,752
FRICK APPLICATION NUMBER: 05/223,762
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FRICK APPLICATION NUMBER: 05/223,762
FRICK APPLICATION NUMBER: 05/223,763
FRICK APPLICATION NUMBER: 05/223,763
FRICK APPLICATION NUMBER: 05/223,763
FRICK FILING DATE: 2000-08-08
FRICK FILING DATE: 2000-08-08
FRICK FILING DATE: 2000-08-14
FRICK APPLICATION NUMBER: 05/225,146
FRICK APPLICATION NUMBER: 05/225,146
FRICK APPLICATION NUMBER: 05/225,392
FRICK APPLICATION NUMBER: 05/225,392
FRICK FILING DATE: 2000-08-15
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US-10-624-932-35
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                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bilerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Stone Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
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Pred. No. 54;
0; Mismatches 1; Indels
                                                                                                                                                                             Grosse, William
Alsobrook, John
Lepley, Denise
Burgess, Catherine
Gerlach, Valerie
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Best Local Similarity 93.3%;
Matches 14; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                        Li, Li
Gusev, Vladimir
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US-10-310-188-57779
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Sequence 1333, Application US/09922181A
GENERAL INFORMATION:
APPLICANT: Gu, Yizhon
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: NGUYEN, CUNG-Tuong
TITLE OF INVANTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ4, MDZ7 AND
FILE REFERENCE: AEOMICA-12
CURRENT APPLICATION NUMBER: US/09/922,181A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOTATION: (2694503)...(2694518)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = US-10-316-954-3538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i LOCATION: (1432166)...(1432181)
i OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber
US-10-316-954-1633
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US-10-316-954-3538/C

1 US-10-316-954-3538/C

1 Sequence 3538, Application US/10316954

2 GENERAL INFORMATION:

3 APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

1 TILE OF INVENTION: Escherichia coli 0157:H7, complete genome.

2 TILE REFERENCE: Jam Zegeer. Law Offices - 703-684-8333

3 CURRENT APPLICATION NUMBER: US/10/316,954

3 CURRENT FILING DATE: 2002-12-12

3 NUMBER OF SEQ ID NOS: 5998

4 SEQ ID NO 3538

5 LENGTH: 16

5 LENGTH: 16
                                                                                                                                                             RESULT 50
US-10-316-954-1633

Sequence 1633, Application US/10316954

Sequence 1633, Application US/10316954

GENERAL INFORMATION:
FAPLICANT Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli 0157:H7, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333

CURRENT PILING DATE: 2002-12-12

NUMBER OF SEQ ID NOS: 5998

SOFTWARE: Proprietary

SEQ ID NO 1633

LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
44.3%; Score 12.4; I
Best Local Similarity 92.9%; Pred. No. 46;
Matches 13; Conservative 0; Mismatches
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                    13 GTACAGGGAGTCCAGG
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Best Local Similarity
Matches 13; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
APPLICANT: Kenneth W. Dobie
FILE OF INVANTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPREFILE SPINE REFERENCE: RTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 105
LENGTH: 20
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Sequence 1341, Application US/09922181A
Sequence 1341, Application
Sequence 134, Application
Sequence 1
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Best Local Similarity 87.5%; Pred. No. 52;
Matches 14; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 87.5%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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47.1%; Score 13.2; 1

Best Local Similarity 83.3%; Pred. No. 58; Matches 15; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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ORGANISM: H. sapiens
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Matches
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US-09-882-945A-275
US-09-882-945A-275
Sequence 275, Application US/09882945A
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor
APPLICANT: Lyamichev, Victor
APPLICANT: Dong, Fang
APPLICANT: Neri, Bruce
APPLICANT: Neri, Bruce
APPLICANT: Neri, Suce
APPLICANT: Neri, Sucieic Acid Accessible Hybridization Sites
FILE REFERENCE: FORS-04586
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Pred. No. 69;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 19;
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Pred. No. 69;
0; Mismatches
APPLICATION NUMBER: 09/032,365
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ORGANISM: Artificial Sequence
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                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity 92.99
Matches 13, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) TOPOLOGY: linear
) MOLECULE TYPE: CDNA
US-09-356-067-30
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TITLE OF INVENTION: BIOINPORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENETITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION WINDER: US/10/310,188
CURRENT FILING DATE: 2022-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTMARE: Patentin version 3.1
SEQ ID NO 32260
LENGTH: 18
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44.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                         14.3%; Score 12.4; DB 1; Length 17; larity 92.9%; Pred. No. 53; Conservative 0; Mismatches 1; Indels
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Sequence 30, Application US/09356067
GENERAL INFORMATION:
APPLICANT: North, Michael
APPLICANT: Nishina, Patsy
APPLICANT: Noben-Trauth, Konrad
APPLICANT: Noben-Trauth, Morente, Suite 200
CITY: Palo Alto
CITY: Palo Alto
CITY: Dalo Alto
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEM: DOS
CURRENT APPLICATION DATA:
PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1333
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 53
US-10-310-188-36260
; Sequence 36260, Application US/10310188
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-36260
                                                                                                                                                               TYPE: DNA
GRGANISM: Homo sapiens
US-09-922-181A-1333
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Best Local Similarity
Matches 13; Conserva
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Gaps
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US-10-303-778-16476/c
US-10-303-778-16476, Application US/10303778
Sequence 16476, Application US/10303778
GENERAL INFORMATION:
TILLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL TILLE OF INVENTION: REGULATORY GENES AND USES THEREOF
TILLE OF INVENTION: REGULATORY GENES AND USES THEREOF
TILLE REFERENCE: 47416
CURRENT APPLICATION UNMER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
SEQ ID NO 16476
LENGTH: 18
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                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT GUO, JINJAGO
1TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
FILE REFERENCE: AEOMICA-31
CURRENT APPLICATION NUMBER: US/60/339,764
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 3310
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2304
LENGTH: 17
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Genealsmance Pharmaceuticals, Inc.
APPLICANT: Geney, Anne
APPLICANT: Choi, Julie Y.
APPLICANT: Koehy, Beena
TILLE OF INVENTION: Haplotypes of the PESI Gene
FILE REFERENCE: MWH-0604PCT PESI
CURRENT APPLICATION NUMBER: PCT/US01/16907
CURRENT APPLICATION NUMBER: 60/203
PRIOR APPLICATION NUMBER: 60/203
PRIOR PILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                      DB 1;
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Pred. No. 6
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Best Local Similarity 82.4°
Matches 14; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGTH: 15
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CORGANISM: Homo sapiens
US-10-303-778-16476
                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2304
                                                        US-60-339-764-2304/c
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PCT-US01-16907-32
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TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
FILE REPERBROCE: AEOMICA-31
CURRENT APPLICATION NUMBER: US/60/339,764
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 3310
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2159
LENGTH: 17
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Pred. No. 57;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/882,945A CTRRENT FILING DATE: 2001-06-15 NUMBER OF SEQ ID NOS: 334 SSEQ ID NO 275 LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-60-339-764-2159/c
; Sequence 2159, Application US/60339764
; GENERAL INFORMATION:
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Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 TGTACAGGGAGTCCAGG
                                                                                                                                                                    ; OTHER INFORMATION: Synthetic US-09-882-945A-275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-60-339-764-2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Matches 14; Conserv
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Gaps
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US-10-719-900-248399/c
; Sequence 248399, Application US/10719900
; Sequence 248399, Application US/10719900
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR RILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 248399
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence:primer US-09-869-169B-2
                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Description of Artificial Sequence:primer US-09-869-169-2
                                                                                                                                                                                                                                                                                                                                                                                                     Length 16;
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APPLICANT: PAULUSSEN, Aimee
APPLICANT: Armstrong, Martin
TITLE OF INVENTION: Genoryping Cytochrome Expression
FILE REFRENCE: 51639/001
CURRENT APPLICATION NUMBER: US/09/869,169B
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: GB 9828619.8
PRIOR APPLICATION NUMBER: GB 9828619.8
PRIOR APPLICATION NUMBER: GB 9828619.8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 16
                 APPLICANT: Armetrong, Martin
TITLE OF INVENTION: Genotyping Cytochrome Expression
FILE REFERENCE: 51539/001
CURRENT APPLICATION NUMBER: US/09/869,169
CURRENT FILING DATE: 2001-06-22
PRIOR PAPLICATION NUMBER: GB 9828619.8
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 57;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Score 11.8; DE Pred. No. 57; 0; Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 86.7%;
Matches 13; Conservative
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Sequence 1332, Application US/09922181A
Sequence 1332, Application US/09922181A
SEQUENCE INFORMATION:
SEQUENCE OF TAXABORY
APPLICANT: Shamon, Mark
APPLICANT: Shamon, Mark
APPLICANT: Shamon, Mark
APPLICANT: Shamon, Mark
TITLE OF INVERTION: CURG-TOOR
FILE REFERENCE: AEOMICA-12
CURRENT APPLICATION NUMBER: US/09/922,181A
CURRENT PILLING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SOGTWARE: Aeomica Sequence Listing Engine
SOGTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1332
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gu, Yizhong
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
APPLICANT: Shannon, Mark
APPLICANT: Nguyen, Cung-Twong
TITLE OF INVENTION: Cung-Twong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ4, MDZ7 AND
FILE REFERENCE. ADOMICA-12
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SSOFTMARE: Acomica Sequence Listing Engine
SSOFTMARE: Acomica Sequence Listing Engine
LENGTH: 17
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                                                                                         Score 12; DB 1; Length 15;
Pred. No. 45;
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61;
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Best Local Similarity 100.0%; Pred. No. 61; Matches 12; Conservative 0; Mismatches
                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                            RESULT 62
US-09-922-181A-1331
; Sequence 1331, Application US/09922181A
; GENERAL INFORMATION:
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                                                                                         42.9%;
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                                                                                                             Best Local Similarity 85.7
Matches 12; Conservative
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-16907-32
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US-09-869-169-2
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                                                                                            Query Match
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                                                                    Sequence 6950, Application US/10287787
GENERAL INFORMATION:
APPLICANT: Feldmann. Richard J.; Global Determinants, Inc., TILLS OF INVENTION: Caulobacter crescentus complete genome: FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,787
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 27958
SOFTWARE: Proprietary
SEQ ID NO 6950
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS-10-287-787-20271/c

Sequence 20271, Application US/10287787

GENERAL INFORMATION:

ARPLICANT: Feldmann, Richard J.; Global Determinants, Inc.;

TITLE OF INVENTION: Caulobacter crescentus complete genome.

FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333

CURRENT FILING DATE: 2003-03-03

NUMBER OF SEQ ID NOS: 27958

SOFTWARE: Proprietary

SEQ ID NO 20271

LENGTH: 15
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GENERAL INFORMATION:
APPLICANT: Dale, Roderic M.K.
APPLICANT: Arrow, Amy
APPLICANT: Thompson, Terry
ITILE OF INVENTION: Homeopathic Anti-Inflammatory;
ITILE OF INVENTION: Compositions
FILE REFERENCE: OLIG-023
CURRENT APPLICATION NUMBER: US/09/590,522
CURRENT PILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11.4; DB
Pred. No. 56;
0; Mismatches
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Pred. No. 56;
0; Mismatches
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; OTHER INFORMATION: Chromosome = 1
US-10-287-787-20271
                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (946131)...(946146)
OTHER INFORMATION: Chromosome
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Best Local Similarity 92.3%;
Matches 12; Conservative (
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Best Local Similarity 92.3%;
Matches 12; Conservative
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US-09-590-522-1
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GENERAL INFORMATION:
APPLICANT: Bradfield, Christopher A.
APPLICANT: Bradfield, Christopher A.
APPLICANT: Bradfield, Christopher A.
APPLICANT: Hogenesch, John B.
TITLE OF INVENTION: CDNAs and Proteins Involved in Hypoxia, Circadian and Orphan Sign;
TITLE OF INVENTION: Transduction Pathways, and Methods of Use
TITLE OF INVENTION: Transduction Pathways, and Methods of Use
TITLE OF INVENTION: Transduction Pathways, and Methods of Use
CURRENT APPLICATION NUMBER: US/09/555,362
CURRENT FILING DATE: 1998-11-27
PRIOR FILING DATE: 1998-11-27
PRIOR FILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin version 3.1
SEQ ID NO 122
LENGTH: 14
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                                                                                             Score 11.8; DB 1; Length 25;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.1%; Score 11.8; DB 1; Length 25; 86.7%; Pred. No. 1.5e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT Xee Mod Zhou TITLE OF INVENTION: Methods of Genetic Analysis of Mouse FILLE REFERENCE: 35.28 CURENT APPLICATION NUMBER: US/60/427,808 CURRENT FILING DATE: 2002-11-20 NUMBER OF SEQ ID NOS: 982914 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 248399 LENGTH: 25
                                                                                                                                                                                                                                                                                                                             US-60-427-808-248399/c
; Sequence 248399, Application US/60427808
; GENERAL INFORMATION:
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                                                                                             42.1%;
86.7%;
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                     8 TACGIGIACAGGGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 TACGTGTACAGGGAG 22
                                                                                                                                                                                                                                     17 TCCCTGTACAGGGAG 3
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Best Local Similarity 86.7
Matches 13; Conservative
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Matches 12; Conservative
                                                                                                                                             Conservative
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CORGANISM: Mus musculus
US-60-427-808-248399
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-248399
                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
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US-09-555-362-122
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RESULT 75
US-09-745-237A-1045/C
Sequence 1045, Application US/09745237A
Sequence 1045, Application US/09745237A
Sequence 1045, Application US/09745237A
Sequence 1045, Application US/09745237A
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (RHEBO0-918-A)
CURRENT FILING DATE: 2002-04-15
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: Patentin version 3.0
SEQ ID NO 1045
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US-09-745-737A-1120/c

US-09-745-237A-1120/c

SGRUERCE 1120, Application US/09745237A

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Batt, Larry

APPLICANT: Batt, Larry

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease

FILE REPRESENCE: 400/007 (MBHB00-918-A)

CURRENT APPLICATION NUMBER: 2002-04-15

NUMBER OF SEQ ID NOS: 4550

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1120

LENGTH 17
                        US-09-745-237A-643/C
US-09-745-237A-643/C
US-09-745-237A-643/C
US-09-745-237A-643/C
SEQUENCE 643, Application US/09745237A
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOPTWARE: Patentin version 3.0
SSP IND 643
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Pred. No. 76;
0; Mismatches
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92.3%; Pred. No. 76;
:ive 0; Mismatches
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 GTGTACAGCGAGT 3
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
COGGANISM: Homo sapiens
US-09-745-237A-643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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; CTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 49626
PCT-USO2-25943-46323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (4497630)...(4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 49627
PCT-US02-25943-46322
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SEQUENCE 46323, Application PC/TUS0225943

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REPRENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICANT: PCT/US02/25943

CURRENT FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 64158

SEQ ID NO 46323

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46322 Application PC/TUS0225943
; Sequence 46322 Application PC/TUS0225943
; GENERAL INFORMATION:
PAPPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT PELLING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SEQ ID NO 46322
; SEQ ID NO 46322
; SEQ ID NO 46322
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
PEATURE:
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
                                                                                                                                                          Score 11.4; I
Pred. No. 66;
0; Mismatches
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.3%;
Matches 12; Conservative
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; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; CRGANISM: homo sapiens
US-09-590-522-1
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Best Local Similarity
Matches 12, Conserva
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PCT-US02-25943-46322/c
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; FEATURE:

; LOCATION: (4497630)...(4497646)

; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 496;

US-10-227-565-46322
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 496;
US-10-227-565-46323
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Mcthod and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MBHBOO, 918-4 400/027
CURRENT APPLICATION NUMBER: US/09/930, 423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: Patentin version 3.0
SEQ ID NO 1120
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US-10-227-565-46322/c

Sequence 46322 Application US/10227565

Sequence 46322 Application US/10227565

GENERAL INFORMATION:

APPLICATION:

PREPLICATION: Pseudomonas aeruginosa PA01, complete genome.

TITLE OF INVENTION: Desendomonas aeruginosa PA01, complete genome.

PILE REPERENCE: Jim Zeger Law Offices - 703-684-8333

CURRENT APPLICATION NUMBER: US/10/227,565

NUMBER OF SEQ ID NOS: 64158

SEQ ID NO 45322

LENGTH: 17
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Desudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CORRENT APPLICATION NUMBER: US/10/227,565
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 46323
LENGTH: 17
LENGTH: 17
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 76;
0; Mismatches
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92.3%; Pred. No. 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GTGTACAGCGAGT 2
                                                                                                                                                                                                                                                                                                              ; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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| Sequence 1045, Application US/09930423
| GENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Blatt, Larry
| TITLE OF INVERTION NUMBER: US/09/930, 423
| CURRENT FILING DATE: 2001-08-15
| NUMBER OF SEQ ID NOS: 4553
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Lart, 
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                                                                     DB 1; Length 17;
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Pred. No. 76;
0; Mismatches
                                                                                                                                      0; Mismatches
                                                                 Score 11.4;
Pred. No. 76;
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; Sequence 1120, Application US/09930423
; GENERAL INFORMATION:
; APPLICANT: Blatt, Larry
; APPLICANT: Blatt, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 643, Application US/09930423; GENERAL INFORMATION:
                                                                 40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.7%;
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                                                                                                  Best Local Similarity 92.3
Matches 12, Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Homo Sapiens
   US-09-745-237A-1120
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-930-423-643/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-930-423-1045
                                                                     Query Match
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) LOCATION: (4497630)...(4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 496;
US-10-367-832A-46323
                                                                FEATURE:
1 LOCATION: (4497630)...(4497646)
2 OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4962
US-10-367-832A-46322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: JOURS, Karen Anne
APPLICANT: JOURS, Karen Anne
APPLICANT: VALDES, Maren Anne
APPLICANT: VALDES, Maren Anne
APPLICANT: VALDES, Maren Anne
APPLICANT: TOWNLEY, David J.
APPLICANT: GALMEY, Nicolas
APPLICANT: GALMEY, Nicolas
APPLICANT: GALMEY, Nicolas
APPLICANT: GALMEY, Alan J.
APPLICANT: GALMEY, Alan J.
APPLICANT: SCHAFER, Alan
TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS ASSOCIATED WITH OSTBOPOROSIS
FILE REFERENCE: PV-0015 PCT
CURRENT APPLICATION NUMBER: US 60/342,711
FRIOR FILING DATE: 2002-12-19
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
SOFTWARE: PERL PROGRAM
SEQ ID NO342
LERGENTH: 16
TURNEY PRIOR FILING DATE: 2002-11-04
SOFTWARE: PERL PROGRAM
SEQ ID NO342
                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-367-832A-46323/c

Sequence 46523, Application US/10367832A

Sequence 46523, Application US/10367832A

Sequence 46523, Application US/10367832A

Sequence 46523, Application US/10363A

TITLE OF INVENTION: Richard J.; Global Determinants, Inc.

TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.

TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.

TITLE OF INVENTION: DATE: 10510/367,832A

CURRENT APPLICATION UNMBER: US/10/367,832A

NUMBER OF SEQ ID NOS: 64158

SOFTWARE: Proprietary

SEQ ID NO 46323

LENGTH: 17
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                                                                                                                                                                                    DB 1; Length 17;
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
                  TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 76;
0; Mismatches
                                                                                                                                                                                    Score 11.4; 1
Pred. No. 76;
                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                  40.7%;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                                                                                                    Query Match
Best Local Similarity
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LENGTH: 17
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Sequence 77630, Application US/10310188

GENERAL INFORMATION:
APPLICANT: RosettaGemonics
APPLICANT: RosettaGemonics
TITLE OF INVENTION: USES THEREOF
TILE REPERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SSOTUMARE: Patentin version 3.1
SEQ ID NO 77530
LENGTH: 17
                                                                                                                                                                               Sequence 68053, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSELEGEMONICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT PAPLICATION NUMBER: 05.02-12-19
NUMBER OF SEQ ID NOS: 86841
SOUTHARRE: Patentin version 3.1
SEQ ID NO 88653
LENGTH: 17
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US-10-367-832A-46322/c
Sguence 46322, Application US/10367832A
SGUENEZAL INFORMATION:
GENERAL INFORMATION:
TILE OF INVENTION: Pseudomonas ascriginosa PA01, complete genome.
TILE OF INVENTION: Pseudomonas ascriginosa PA01, complete genome.
TILE OF INVENTION: Decer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
SOFTWARRE: Proprietary
SOFTWARE: Proprietary
SOFTWARE: Proprietary
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Pred. No. 76;
0; Mismatches
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Mismatches
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Best Local Similarity 92.3%;
Matches 12; Conservative
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12; Conservative
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US-10-310-188-77630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-10-310-188-68063
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Matches
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Query March 40.0%; Score 11.2; DB 1; Length 16; Best Local Similarity 81.2%; Pred. No. 71; Matches 13; Conservative 0; Mismatches 3; Indels
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Sequence 23, Application PC/TUS9503316
Sequence 23, Application PC/TUS9503316
Sequence 23, Application
INFORMATION:
APPLICANT: Kamb, Alexander
ITILE OF INVENTION: GENE, AND METHODS FOR DIAGNOSIS, PROGNOSIS AND THERAPY OF
ITILE OF INVENTION: CANCER DUE TO THE MTS GENE
INUMBER OF SEQUENCES: 36
CORRESPONDENCES: 36
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                              Length 16;
; FEATURE:

; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: NOT304 B Primer Sequence
PCT-USO2-40948-348
                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005

COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATI APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
                                                                                                                                        Query Match
40.0%; Score 11.2; DB 1;
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 01-UNN-1994
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/215,088
FILING DATE: 18-MAR-1994
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/214,581
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,581
FILING DATE: 14-APR-1994
FRICK APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
FRICK APPLICATION NUMBER: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,609
REGISTRATION NUMBER: 38,609
REGISTRATION NUMBER: 38,609
REGISTRATION NUMBER: 38,609
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                           11 GTGTACAGGGAGTCCA 26
                                                                                                                                                                                                                                                                                                                  16 GAGTCCAGCGAGTCCA 1
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DB 1;
                                                                                                                                                                                                                         40.0%; Score 11.2;
                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
1 cererciaesasecc 16
                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                        nucleic aci
                                                                                                                                                                                                         ; ANTI-SENSE: YEE; ORIGINAL SOURCE: ; ORGANISM: Hon PCT-US95-03537-23
                                                                                                                                                                                           STRANDEDNESS:
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Gaps . 0

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              Indels
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 81.2%; Pred. No. 71;
iive 0; Mismatches
Best Local Similarity 81.2
Matches 13, Conservative
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DB 1; Length 16; Indels COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
OPERATION SYSTEM: PC-D05/M5-D05
SOFTWARE: Patentin Release #1.0, Version #1.30
CULASSITIONING SYSTEM: US 08/479,731
FILING DATE: 07-JUN-1995
FILING DATE: 17-MR-1995
FRIOR APPLICATION NUMBER: US 08/251,938
FRIOR APPLICATION NUMBER: US 08/251,938
FRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
FRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
FRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
FRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 19-MAR-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 19-MAR-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 19-MAR-1994
FRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 19-MAR-1994
FRIOR APPLICATION NUMBER: 28/957
FREEFRACE/DOCKET NUMBER: 28/957 Query Match
40.0%; Score 11.2; D
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHERICAL: NO ANTI-SENSE: YES 10 CGTGTACAGGGAGTCC 25 1 cererciaeaaece 16 쉽 APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PLOPDY disk
COMPUTER: PLOPDY DASH
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PACHALIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIPICATION: 435 24884-109348-G CLASSIFICATION 943APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: 28,957
REPERENCE/DOCKET NUMBER: 38,957
REPERENCE/DOC US-08-474-083-23 Sequence 23, Application US/08474083 GENERAL INFORMATION: 10 CGIGIACAGGGAGICC 25 1 cererceaseasece 16 HYPOTHETICAL: NO
HYPOTHETICAL: NO
HANT-SENSE: YES
ORIGINAL SOURCE:
CRGANISM: HOMO
US-08-474-083-23

Gaps ö 40.0%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 71; tive 0; Mismatches 3; Indels RESULT 90

US-08-479-731-23

SEQUENCE 23, Application US/08479731

SEQUENCE 23, Application US/08479731

SEDIEGANT: Kamb, Alexander

TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC. Query Match Best Local Similarity 81.2 Matches 13; Conservative

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1 CCACCAGUACAGGGAG 16
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1 CGTGTCCAGGAAGCCC 16
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Best Local Similarity 81.2
Matches 13; Conservative
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CORGANISM: Homo sapiens
PCT-US02-16840-1766
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         US-10-310-188-34900
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40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                           CALF: AUGUS

CAMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MR-1995
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 10-JUN-1994
FILING DATE: 18-MR-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MR-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MR-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
PRICK APPLICATION NUMBER: US 08/214,582
FILING DATE: 14-APR-1994
PRICK APPLICATION NUMBER: US 08/214,582
FILING DATE: 11-APR-1994
PRICK APPLICATION NUMBER: US 08/214,582
FILING DATE: 11-APR-1994
ATTORNEY/AGANT INPORMATION:
NAME: Inhen, Jeffrey.
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                  10 CGTGTACAGGGAGTCC 25
                                               1 CGTGTCCAGGAAGCCC 16
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                                                                                                                                               US-08-481-063-23
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10 CGTGTACAGGGAGTCC 25

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Sequence 1766, Application PC/TUS0216840

Sequence 1766, Application PC/TUS0216840

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Macleic Acid Treatment of Diseases or Conditions Related to Leve
TITLE OF INVENTION: Macleic Acid Treatment of Diseases or Conditions Related to Leve
TITLE OF INVENTION: Macleic Acid Treatment of Diseases or Conditions Related to Leve
TITLE OF INVENTION: Macleic Acid Treatment of Diseases or Conditions Related to Leve
TITLE OF INVENTION WHER: PCT/US02/16840
CURRENT APPLICATION NUMBER: US 60/296,249
PRIOR FILING DATE: 2001-05-10
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 6810
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1766
Sequence 34900, Application US/10310188

SEGUENCE 34900, Application US/10310188

GENERAL INFORMATION:
TYPILE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
TYPILE OF INVENTION: USES THEREOF
TYPILE OF INVENTION: US/10/310,188
CURRENT APPLICATION WUNDER: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 34900
LENGTH: 16
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; Sequence 1766, Application PC/TUS0216840A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic, Acid Treatment of Diseases or Conditions Related to Leve
; TITLE OF INVENTION: RAS, HER2 and HIV
; FILE REPERENCE: 400/046 (MBHB02-326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 71; 1; or 0; Mismatches 3; Indels
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Sequence 2951, Application US/09018875

Sequence 2951, Application US/09018875

Sequence 2951, Application US/09018875

SEGUENCRAL INFORMATION:

APPLICANT: Kmiec, Eric B.

APPLICANT: Race, Michael C.

TILE OF INVENTION: Targed Cd. Chromosomal Genomic Alterations with Modified Single

TILE OF INVENTION: Stranded Oligomucleotides

TILE OF INVENTION: Stranded Oligomucleotides

FILE REPRENCE Napro-

CURRENT APPLICATION NUMBER: US/09/818,875

CURRENT FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR PELING DATE: 2000-03-27

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: US 60/208,538

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR FILING DATE: 2000-06-01

PRIOR SEQ ID NOS: 4386

SOFTWARE: Friedman macro Napro4

LEMANDARY: TARGED TO 2000-06-01

PRIOR APPLICATION OF 1386

SEQ ID NO 2951
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APPLICANT: GU, Yizhong
APPLICANT: Sharnon, Mark
APPLICANT: Sharnon, Mark
APPLICANT: Sharnon, Cung-Tuong
TITLE OF INFORMATION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 ANI
FILE REPERBNCE: AEOMICA-12
CURRENT APPLICATION NUMBER: US/09/922,181A
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SOFTWARE: Aeomica Sequence Listing Engine
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Pred. No. 82;
0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SEQ ID NO 2950
SEQ ID NO 2950
LENGTH: 17
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Sequence 1343, Application US/09922181A
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Best Local Similarity 81.2%;
Matches 13; Conservative
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Best Local Similarity 81.2%;
Matches 13; Conservative
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US-09-818-875-2951
                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-09-818-875-2950
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APPLICANT: Kmiec, Eric B.
APPLICANT: Kmiec, Eric B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-4
CURRENT FILING DATE: 2001-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR PAPLICATION NUMBER: US 60/192,176
PRIOR PAPLICATION NUMBER: US 60/192,179
PRIOR PLING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blatt, larry
APPLICANT: Zwick, Michael
APPLICANT: Pavoc, Pam
APPLICANT: McSwiggen, Jim
TITLE CANT: McSwiggen, Jim
FILE REFERENCE: 237/193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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40.0%; Score 11.2; I
Best Local Similarity 62.5%; Pred. No. 82;
Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
               CURRENT APPLICATION NUMBER: PCT/US02/16840A
                                                                                                                                                                                                                                                                                                                                                                                                          40.0%; Score 11.2; 75.0%; Pred. No. 82
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CURRENT FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 7043
SOFTWARE: Patentin version 3.0
SEQ ID NO 6677
LENGTH: 17
                                                    PRIOR APPLICATION NUMBER: US 60/318,471
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 60/296,249
PRIOR APPLICATION NUMBER: US 60/294,140
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 6810
SOFWARE: Patentin version 3.0
SEQ ID NO 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Blatt, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6677, Application US/09546745A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 CTACGTGTACAGGGAG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CTACGTGTACAGGGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ccaccaguacaggagg 16
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                           TYPE: RNA
CORGANISM: Homo sapiens
PCT-US02-16840A-1766
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US-09-818-875-2950/c
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Sequence 2951, Application US/10209787

Sequence 2951, Application US/10209787

GENERAL INFORMATION:

APPLICANT: KEMIAC. Exic B.

APPLICANT: Genger, Howard B.

APPLICANT: Genger, Howard B.

APPLICANT: Application US/10209.787

TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single

TITLE OF INVENTION: Stranded Oligonucleotides

FILE REFERENCE: Napro-730

FILE REPERENCE: 2002-07-30

FILE REPERENCE: 2001-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR APPLICATION NUMBER: US 60/192,179

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR PELING DATE: 2000-06-01

PRIOR
APPLICANT: Kmiec, Eric B.
APPLICANT: Gamper, Howard B.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides
FILE REPERENCE: Napro-4
CURRENT APPLICATION NUMBER: US 09/618,875
PRIOR APPLICATION NUMBER: US 09/618,875
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR APPLICATION NUMBER: US 60/204,538
PRIOR PRIOR APPLICATION NUMBER: US 60/204,538
PRIOR APPLICATION NUMBER: US 60/204,538
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81.2%; Pred. No. 82;
tive 0; Mismatches 3;
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Pred. No. 82;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 ACCTGTACAGGGAGTC 24
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; ORGANISM: Homo sapiens
US-10-209-787-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Homo sapiens
US-10-209-787-2950
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Matches 13; Conserv
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Sequence 7027, Application US/10156306
Sequence 7027, Application US/10156306
Sequence 7027, Application US/10156306
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSWiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and FKR
FILE REFERENCE: MHB01-64-A (400/050)
CURRENT PILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: Patentin version 3.0
SEQ ID NO 7027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ribosyme Pharmaceuticals, Inc.
APPLICANT: Ribosyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REPERENCE: MUMBER: US/10/156,306
CURRENT APPLICATION NUMBER: US/10/156,306
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: Patentin version 3.0
SEQ ID NO 7026
LENGTH: 17
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                                                                                                                                                                  Query Match
40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels
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68.8%; Pred. No. 82;
tive 2; Mismatches
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18-10-209-299-2950/c

; Sequence 2950, Application US/10209787

; GENERAL INFORMATION:
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2.10-156-306-7026
; Sequence 7026, Application US/10156306
; GENERAL INFORMATION:
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Best Local Similarity 68.8
Matches 11, Conservative
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CORGANISM: Homo sapiens
US-10-156-306-7027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: RNA; ORGANISM: Homo sapiens
US-10-156-306-7026
                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11, Conserva
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GENERAL INFUGENTION:

APPLICANT: Kaniec, Eric B.
APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: NaPro-4CON
CURRENT FILING DATE: 2002-09-27
FRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/244,989
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GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT PILING DATE: 202-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 41474
LENGTH: 17
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GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTIFLE OF INVENTION: USES THERROF
FILE REPRENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
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llarity 81.2%; Pred. No. 82;
Conservative 0; Mismatches
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Sequence 2951, Application US/10261185
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B1.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
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US-10-310-188-41474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-10-261-185-2951
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US-10-310-188-74621/c
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US-10-310-188-41474
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Matches 13; C
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Sequence 2950, Application US/10261185
GENERAL INFORMATION:
APPLICANT: Kaiec, Eric B.
APPLICANT: Kaiec, Eric B.
APPLICANT: Raiec, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single FILE REFERENCE: Napro-4CNN
FILE OF INVENTION: Stranded Oligonucleotides
FILE REPERENCE: Napro-4CNN
CURRENT APPLICATION NUMBER: US/10/261,185
CURRENT APPLICATION NUMBER: US/02-09-27
CURRENT APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-06-01
SPRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
SPRIOR FILING DATE
                                                                   Sequence 3087, Application US/10238700
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwidgen, James
APPLICANT: McSwidgen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
FILE REFERENCE: 400/057 (MBH801-1158-A)
CURRENT APPLICATION NUMBER: US/10/238,700
CURRENT APPLICATION NUMBER: PCT/US 02/16840
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 4666
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3087
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Pred. No. 82;
0; Mismatches
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1 Similarity 75.0%; Pred. No. 82;
12; Conservative 1; Mismatches
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Best Local Similarity 81.2%; Pr
Matches 13; Conservative 0;
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US-10-261-185-2950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
CORGANISM: Homo sapiens
US-10-238-700-3087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 12; Conserv
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US-10-261-185-2951
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Sequence 2080, Application US/10605840
| Sequence 2080, Application US/10605840
| Sequence 2080, Application Sequence 2080, Seque
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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-471-271-2305
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Sequence 2950, Application US/10623107

Sequence 2950, Application US/10623107

GENERAL INFORMATION:

TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL

TITLE OF INVENTION: OLICONUCLEOTIDES

TITLE OF INVENTION: OLICONUCLEOTIDES

CURRENT APPLICATION NUMBER: US/10/623,107

CURRENT FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-19

NUMBER OF SEQ ID NOS: 7046

SOFTWARE: Patentin ver 3.2

SEQ ID NO 2950
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Best Local Similarity 68.8%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches
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Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches
             CURRENT APPLICATION NUMBER: US/10/471,271
                           CURRENT FILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-04-05
PRIOR PILING DATE: 2001-04-05
PRIOR PILING DATE: 2001-05-9
PRIOR APPLICATION NUMBER: 60/294,412
PRIOR APPLICATION NUMBER: 60/294,315
PRIOR PILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-08-26
NUMBER OF SEQ ID NOS: 13274
SOFFWARE: PATENTIN VERSION 3:0
SEQ ID NO 2305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Artificial Sequence
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CRGANISM: Homo sapiens
US-10-605-840-2080
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US-10-605-840-2080/c
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US-10-471-271-2304

US-10-471-271-2304

Sequence 2304, Application US/10471271

Sequence 2304, Application US/10471271

Sequence 2304, Application US/10471271

APPLICANT: Blact. Lawrence

APPLICANT: Haeberli, Perer

APPLICANT: Mediation of Gene Expression Associated with Inflammation Prolif

TITLE OF INVENTION: Modulation of Gene Expression Associated with Inflammation Prolif

TITLE OF INVENTION: Modulation of Gene Expression Associated with Inflammation Prolif

TITLE OF INVENTION: And Neurite Growth Using Nucleic Acid Based Technologies

TITLE OF INVENTION: MOMBER: US/10/471,271

CURRENT APPLICATION NUMBER: 09/0-05

PRIOR PELING DATE: 2001-02-05

PRIOR PELING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 09/827,395

PRIOR APPLICATION NUMBER: 09/827,395

PRIOR APPLICATION NUMBER: 09/827,395

PRIOR APPLICATION NUMBER: 00/315,315

PRIOR APPLICATION NUMBER: 00/315,315
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Sequence 2305, Application US/10471271
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: Haeberli, Peter
APPLICANT: Haeberli, Peter
APPLICANT: Hospidgen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Modulation of Gene Expression Associated with Inflammation Prolif
TITLE OF INVENTION: and Neurite Growth Using Nucleic Acid Based Technologies
FILE REFERENCE: MSHB 02-258-PCT (400/045)
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US-10-471-271-2304
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Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 74621
LENGTH: 17
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Homo sapiens
US-10-310-188-74621
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TYPE: RNA
CORGANISM: Homo sapiens
US-10-724-270-1766
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Sequence 2950, Application US/10681074

Sequence 2950, Application US/10681074

Sequence 2950, Application US/10681074

APPLICANT: WANEK, ENIC B.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN

TITLE OF INVENTION: OLIGONUCLECTIED NUCLEIC ACID SEQUENCE ALTERATION

TITLE OF INVENTION: OLIGONUCLECTIED NUCLEIC ACID SEQUENCE ALTERATION

CURRENT FILING DATE: 2003-10-07

PRIOR FILING DATE: 2003-03-07

PRIOR FILING DATE: 2003-03-07

NUMBER OF SEQ ID NOS: 4375

SOFTWARE: PATENTIN OF SEQ ID NOS: 4375

LENGTH: 17
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US-10-623107-2951
US-10-623107-2951
SQUENCE 2951, Application US/10623107
GENERAL INFORMATION:
JAPPLICAMY: WILE, BEITC B.
TITLE OF INVENTION: OLIGONUCLECTIDES
JTITLE OF INVENTION: OLIGONUCLECTIDES
JTITLE OF INVENTION: OLIGONUCLECTIDES
JTITLE OF INVENTION: OLIGONUCLECTIDES
JETLE REPERBENCE:
JETLE PEPERBENCE:
JETLE OF INVENTION: UNMERR: US/10/623,107
CURRENT APPLICATION NUMBER: US 60/397,555
JETLE APPLICATION NUMBER: US 60/397,555
JETLE OF INVENTION DATE: 2003-07-19
NUMBER OF SEQ ID NOS: 7046
JENGTH:
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40.0%; Score 11.2; I
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches
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81.2%; Pred. No. 82;
tive 0; Mismatches
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Matches 13; Conservative
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CRGANISM: Homo sapiens
US-10-623-107-2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-2950
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Matches 13; Conserv
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US-10-681-074-2950/c
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US-10-724-270-1766

J. Sequence 1765, Application US/10724270

GENERAL INFORMATION:

APPLICANT: Star Therapeutics, Inc.

APPLICANT: Star Therapeutics, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: Uncleic Acid Treatment of Diseases or Conditions Related to Leve

TITLE OF INVENTION: Uncleic Acid Treatment of Diseases or Conditions Related to Leve

TITLE OF INVENTION: RAS, HERZ and HIV.

CURRENT FILING DATE: 2003-11-26

FRIOR FILING DATE: 2003-11-26

PRIOR FILING DATE: 2001-05-10

PRIOR FILING DATE: 2001-05-10

PRIOR FILING DATE: 2001-05-10

PRIOR FILING DATE: 2001-05-20

PRIOR FILING DATE: 2003-04-16

PRE
Sequence 2951, Application US/10681074

GENERAL INFORMATION:
APPLICANT: WAIG. ERIC B.
APPLICANT: WAIG. ERIC B.
TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
FILE REPERRNCE: NaPro-18 US
CURRENT APPLICATION NUMBER: US/10/681,074
CURRENT APPLICATION NUMBER: US 60/453,360
PRIOR PILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 4375
SEQ ID NOS: 4375
LENGTH: 17

LENGTH: 17
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40.0%; Score 11.2; D
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
US-10-681-074-2951
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; SEQ ID NO 2303
; LENGTH: 17
; TYPE: DNA
; CRGANISM: Homo sapiens
US-60-339-764-2303
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LENGTH: 17
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US-60-339-764-2160/c
Sequence 2160, Application US/60339764
GENERAL INFORMATION:
APPLICANT: GUO, JINJIAO
TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
CURRENT APPLICATION NUMBER: US/60/339,764
CURRENT PILLOATION NUMBER: US/60/339,764
NUMBER OF SEQ ID NOS: 3310
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2160
LENGTH: 17
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GENERAL INFORMATION:
APPLICANT: Guo, Jinjiao
TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
FILE REFERENCE: AEOMICA-31
CURRENT APPLICATION NUMBER: US/60/339,764
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 3310
SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                          Length 17;
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                 DB 1;
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Best Local Similarity 81.2%; Pred. No. 92;
Matches 13; Conservative 0; Mismatches
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Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches
              Query Match 40.0%; Score 11.2; I Best Local Similarity 75.0%; Pred. No. 82; Matches 12; Conservative 1; Mismatches
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1 CCACCAGUACAGGGAG 16
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                                                                               7 CTACGTGTACAGGGAG 22
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CRGANISM: Homo sapiens
US-60-339-764-2160
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; ORGANISM: Homo sapiens
US-60-339-764-2158
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US-60-339-764-2303/c
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LOCATION: (845005)...(845019)

CHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 132
US-10-305-275-941
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                                                                                                                                                                                                                                                           Sequence 2305, Application US/60339764
GENERAL INFORMATION:
APPLICANT: Guo, Jinjian
TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
FILE REPERENCE: AEOMICA-31
CURRENT APPLICATION NUMBER: US/60/339,764
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 3310
SOFTWARE: Aeomica Sequence Listing Engine
     DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 17;
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39.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                  Indels
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GENERAL INFORMATION:
APPLICANT: Peldmann. Richard J.; Global Determinants, Inc., ITLLE OF INVENTION: Aeropyrum pernix K1 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-11-28
NUMBER OF SEQ ID NOS: 1617
SEQ ID NO 941
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Aeropyrum pernix Kl complete genome.
FEATURE:
Query Match 40.0%; Score 11.2; D
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches
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Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches
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US-10-305-275-942/c
; Sequence 942, Application US/10305275
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                                                                                                  6 CCTACGTGTACAGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRCANISM: Homo sapiens
US-60-339-764-2305
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Sequence 56454, Application US/10310188

GENERAL INFORMATION:
APPLICANT: ROSettademonics
APPLICANT: ROSettademonics
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE REPRENCE: 47487
CURRENT PILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86441
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
SEQ ID NO 56454
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PCT-USO1-44838-5/c
Sequence 5, Application PC/TUSO144838
Sequence 5, Application PC/TUSO144838
Sequence 5, Application PC/TUSO144838
TILE OF INVENTION:
TILE OF INVENTION: Genetic Typing of Human Genes And Related Materials And Methods
FILE REFERENCE: 4389-23-PCT
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 1449
SOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
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GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Egeger Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25943
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                                              Length 15;
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Pred. No. 71;
0; Mismatches 2;
                                              Score 11; DB 1;
Pred. No. 66;
                                  39.3%; bccd. No. c. 100.0%; Pred. No. c. 0; Mismatches
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85.7%;
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Best Local Similarity luv...
Local Similarity luv...
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Local Similarity
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                                                 Query Match 39.3
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                          18 GGGAGTCCAGG 28
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CORGANISM: Homo sapiens
PCT-US01-44838-5
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CORGANISM: Homo sapiens
US-10-310-188-56454
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Best Local Similarity
Matches 12; Conserv
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PCT-US02-25943-41393/c
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US-10-310-188-56454
  US-10-305-275A-942
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LOCATION: (845005)...(845019)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1328
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1. LOCATION: (845005)...(845019)
1. OCHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1329
US-10-305-275A-941
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US-10-305-275A-942/C
; Sequence 942, Application US/10305275A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.; TITLE OF INVENTION:
; TILE OF INVENTION: Acropyrum pernix Xi complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,275A
; CURRENT FILING DATE: 2002-11-27
; SOFTWARE: Proprietary
; SOFTWARE: Proprietary
; SEQ ID NO 942
; LENGTH: 15
; TYPE: DNA
; GRANISM: Aeropyrum pernix XI complete genome.
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WS-10-375A-941/c
| Sequence 941, Application US/10305275A
| GENERAL INFORMATION: APPLICATION | APPLICAMY: Reldmann, Richard J.; Global Determinants, Inc. | APPLICAMY: Reldmann, Richard J.; Global Determinants, Inc. | TITLE OF INVENTION: Aeropyrum pernix K1 complete genome. | FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333 | CURRENT APPLICATION WINBER: US/10/305,275A | CURRENT PILING DATE: 2002-11-27 | NUMBER OF SEQ ID NOS: 1617 | SSCTIMARE: Proprietary | SSCTID NO 941 | LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.3%; Score 11; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 66; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.3%; Score 11; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 66; Matches 11; Conservative 0; Mismatches 0; Indels
GENERAL INFORMATION:

APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
IIILE OF INVENTION: Aecopyrum pernix K1 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/305,275
CURRENT FILING DATE: 2002-11-28
NUMBER OF SEQ ID NOS: 1617
SEQ ID NO 942
LENGTH: 15
                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Aeropyrum pernix K1 complete genome.
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ORGANISM: Aeropyrum pernix K1 complete genome.
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, OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553B-143
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Pred. No. 71;
2; Mismatches 2;
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US-09-274-553B-143
; Sequence 143, Application US/09274553B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4%;
Matches 10; Conservative
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; ORGANISM: Hepatitis C Virus
US-09-274-553-678
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      GGGCCCTACGTGTA 15
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                                   GGGCCCUCCGUGCA 14
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                                                                                                                                                                                                                           2; Indels
                                                                               TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HEPATITIS C TITLE OF INVENTION: INHIBITING HEPATITIS C TITLE OF INVENTION: INHIBITING HEPATITIS C TITLE OF INVENTION: VIRUS REPLICATION CRRESPONDENCES: 497
CORRESPONDENCES: 100
COMPUTER: 03.0
COMPUTER: California
COMPUTER: 103.6
COMPUTER: 104 Mb
MEDIUM TYPE: 3.5"
MEDIUM TYPE: 5.0
CORPUTER: 104 Mb
MEDIUM TYPE: 105.6
COMPUTER: 105.6
COMPUTER: 105.6
CORPUTER: 105.6
CORPUTER: 105.6
CORPUTER: 105.6
CORRENT APPLICATION DATA: 106.7
FILING DATE: 106.7
APPLICATION NUMBER: 06/182,968
FILING DATE: 13.7
APPLICATION NUMBER: 06/182,968
FILING DATE: 13.7
APPLICATION NUMBER: 07/882,888
FILING DATE: 14.4
APPLICATION NUMBER: 205/277
REGISTRATION NUMBER: 205/277
REGISTRATION NUMBER: 205/277
REGISTRATION NUMBER: 205/277
RESPERENCE/DOCKET NUMBER: 205/277
                                                                                                                                                                                          Score 10.8; Di
Pred. No. 71;
0; Mismatches
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38.6%; Score 10.8; 1
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Sequence 121, Application US/08774306
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
     2002-08-27
64158
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 121
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                        13 GTACAGGGAGTCCA 26
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STRANDEDNESS: sing
CURRENT FILING DATE: 2
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PROPRIECARY
SEQ ID NO 41393
LENGTH: 15
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GENERAL INFORMATION

JAPPLICANT: Blatt, Lawrence

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Pacco, Pamela

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

FILE REFERENCE: DISPONDING NUMBER: US/09/274,553E

CURRENT FILING DATE: 1999-02-24

PRIOR FILING DATE: 1999-04-27

PRIOR PLING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3148

SOFTWARE: Patentin version 3.0

SEQ ID NO 143

LENGTH: 15
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GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: Roberts, Ben,
APPLICANT: Roberts, Ben,
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Macejak, Dennis
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE SPERENCE: TPI 247/282
CURRENT APPLICATION NUMBER: US/09/504,231A
CURRENT FILING DATE: 2000-02-15
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US-09-274-553E-143
                                    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-143
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                                                                                                                                                       Score 10.8; DB 1; Length 15; Pred. No. 71; 2; Mismatches 2; Indels
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Pred. No. 71;
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2; Mismatches
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PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR PILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                                                                  Query Match 38.6%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.6%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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US-09-504-231A-143
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US-09-274-553E-143
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Sequence 1143, Application US/09274553D

SERVERAL INPORMATION:
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Macelsk, Dennis
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REFERENCE: FD 247/282
CURRENT APPLICATION NUMBER: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1999-09-16
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1999-09-16
PRIOR FILING DATE: 1999-09-16
PRIOR FILING DATE: 1999-09-16
SPRIOR FILING DATE: 1999-09-
                                                                                                                                                                                                                                                                                                                                                  Sequence 143, Application US/09274553C

Sequence 143, Application US/09274553C

Sequence 143, Application US/09274553C

Sequence 143, Application US/09274553C

APPLICANT: Blatt, Lawrence

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Macejab, Dennia

APPLICANT: Macejab, Dennia

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

FILE REFERENCE: P19 247, 242

CURRENT APPLICATION NUMBER: US/09/274,553C

CURRENT APPLICATION NUMBER: 05/257,608

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3148

SOFTWARE: PatentIn version 3.0

SEQ ID NO 143

LENGTH: 15
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US-09-274-553C-143
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Pred. No. 71;
2; Mismatches 2; Indels
   DB 1; Length 15;
                                                                        2; Indels
       Score 10.8; Di
Pred. No. 71;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 71.4%;
Matches 10; Conservative
       Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGCCCTACGTGTA 15
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NESOUR 138

Sequence 143. Application US/09611931A

Sequence 143. Application US/09611931A

Sequence INFORMATION:

APPLICANT: Blatt, Lawrence

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Macejak, Dennis

TITLE OF INVENTION: ENZYMATIC UVCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELA'

TITLE OF INVENTION: ENZYMATIC US/09/611,931A

TITLE OF INVENTION: ENZYMATIC US/09/611,931A

TITLE OF INVENTION: ENZYMATIC OF 18/09/611,931A

TITLE OF INVENTION: ENZYMATIC OF 18/09/611,931A

CURRENT FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3242

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-611-931-143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.6%; Score 10.8; DB 1; Length 15; Best Local Similarity 71.4%; Pred. No. 71; Matches 10; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15
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           HEPATITIS C VIRUS INFECTION
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                          TILE DE TRIVELLION.

FILE REFERENCE: TPJ 250/285

CURRENT APPLICATION NUMBER: US/09/611,931

CURRENT FILING DATE: 2001-04-09

PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: 09/257,608

PRIOR APPLICATION NUMBER: 60/100,842

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1998-04-18

PRIOR FILING DATE: 1998-04-18

PRIOR FILING DATE: 1998-04-18

PRIOR FILING DATE: 1998-04-18

SOSTWARE: PALENTIN NUMBER: 60/083,217

PRIOR FILING DATE: 1998-04-27

SOSTWARE: PALENTIN VOIS: 3242

SEQ ID NO 143

LENGTH: 155

LENGTH: 155
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US-09-633-515-121
; Sequence 121, Application US/09633515
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Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-611-931A-143
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Sequence 143. Application US/09504231B
SEQUENCE INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Damela
APPLICANT: Wording, Damela
APPLICANT: Wording In HEARITIS C VIRUS INFECTION
FILE REFRENCE: Rabboolen, A (247/282)
CURRENT APPLICATION NUMBER: U9/09/504,231B
CURRENT APPLICATION NUMBER: 09/274,553
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3258
SEQ ID NO 143
FRIDK PLING DATE: 1998-04-27
SOUTHAND: APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
SOUTHAND: PRIOR PLING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3258
SEQ ID NO 143
FRIDK PLING DATE: 1998-04-27
SEQ ID NO 143
FRIDK PLING DATE: 1998-04-27
FRIDK PLING DATE: 1998-04-27
NUMBER OF SEQ ID NO 143
FRIDK PLING DATE: 1998-04-27
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GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Dennis
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
                                                                                                                                                                                                                                              TYPE: RNA ORGANISM: Artificial Sequence PERTURE: ORGANISM: Artificial Sequence: Nucleic Acid Target US-09-504-231A-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
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Pred. No. 71;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION UMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3242
SOFTWARE: PatentIn version 3.0
LENGTH: 15
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4%;
Matches 10; Conservative
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. LOCATION: (4017819)...(4017834)
) OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 4432
US-10-227-565-41393
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US-10-186-34441
Squence 34441, Application US/10310168
; SEQUENCE 34441, Application:
; PENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . LOCATION: (4017819)...(4017834)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 443
US-10-367-832A-41393
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US.10-227-565-41393/C

Sequence 41393, Application US/10227565

Sequence 41393, Application US/10227565

SEQUENCE AL INPORMATION:
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFRENCE: Jim Segeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-08-26

NUMBER OF SEQ ID NOS: 64158

SOFTWARE: Proprietary

SEQ ID NO 41393

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41393, Application US/10367832A
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Beaudomonas aeruginosa PA01, complete genome.
FILE REFRENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 41393
LENGTH: 15
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                      38.6%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 71; 2:ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10.8; D
Pred. No. 71;
0; Mismatches
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Pred. No. 71;
0; Mismatches
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                    15 ACAGGGAGTCCAGG 28
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Query Match
Best Local Similarity 85.77
Conservative
                                                                                                                                                         15 ACAGGGTTTCCAGG 2
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Best Local Similarity 85.7%
Matches 12, Conservative
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US-10-367-832A-41393/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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                                APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HEPAITIS C TITLE OF INVENTION: VINUS REPLICATION NUMBER OF SEQUENCES: 498
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 138
US-09-724-389-5/c
Sequence 5, Application US/09724389
SEQUENCE 5, Application US/09724389
SEQUENCE 5, Application US/09724389
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/724,389
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 1449
SEQ ID NO 5
LENGTH: 15
TYPE: DATE
CORRANTEN: Patentin version 3.0
SEQ ID NO 5
LENGTH: 15
CORGANISM: Homo sapiens
US-09-724-389-5
                                                                                                                                                                                                                                                                                                                 ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: Disk Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/633,515
FILING DATE: 2000-08-07
APPLICATION NUMBER: 09/064,156
FILING DATE: January 13, 1994
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,968
FILING DATE: MAN 14, 1992
ATTONEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPRENENC/COCKET NUMBER: 234/083
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGGCCCTACGTGTA 15
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STRANDEDNESS: single
                                                                                                                                                                                                                                               Los Angeles
3: California
RY: U.S.A.
90071-2066
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                 GENERAL INFORMATION:
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Gaps
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APPLICANT: Genaissance Pharmaceuticals, Inc.
APPLICANT: Chew, Anne
APPLICANT: Chew, Anne
APPLICANT: Pinkel, Kevin
APPLICANT: Finkel, Kevin
APPLICANT: Finkel, Kevin
APPLICANT: Han, Jin-Hua
APPLICANT: Haser, Chad
APPLICANT: Harell, Charles
TITLE OF INVENTION: HAPLOTYPES OF THE ADH4 GENE
FILE REPRENCE: ADH4 WMH1088-PCT
CURRENT APPLICATION NUMBER: 60/227,816
FRIOR FILING DATE: 2001-08-22
FRIOR FILING DATE: 2000-08-25
FRIOR FILING DATE: 2000-08-25
FRIOR FILING DATE: 2000-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Amstadio, Alison E. APPLICANT: Amstadio, Alison E. APPLICANT: Niew, Stefanie E. APPLICANT: Kliew, Stefanie E. APPLICANT: Koshy, Beena APPLICANT: Sausker, Elizabeth Ann TILLE OF INVENTION: Haplotypes of the CFLI Gene FILE DEFERENCE: MMH-0706FCT CFLI CURRENT APPLICATION NUMBER: PCT/US01/18815 CURRENT FILING DATE: 2010-06-11 PRIOR PILING DATE: 2000-06-09 NUMBER OF SEQ ID NOS: 65 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 7 LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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GENERAL INFORMATION:
APPLICANT: Genaissance Pharmaceuticals, Inc.
APPLICANT: Anastasio, Alison E.
                                                                                                                                                                            Score 10.4;
Pred. No. 47;
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Pred. No. 82
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                                                                      FEATURE:
; OTHER INFORMATION: mutated pUC19
US-10-407-637-20
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SOFTWARE: Patentin version 3.1
SEQ ID NO 16
TRNTH: 15
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ilarity 78.6%;
Conservative
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                         TYPE: DNA
ORGANISM: unknown
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LENGTH: 12
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Sequence 20, Application PC/TUS0310296

Sequence 20, Application PC/TUS0310296

GENERAL INFORMATION:

APPLICATT: New England Biolabs, Inc.

TITLE OP INVENTION: Methods And Compositions For DNA Manipulation

FILE REPERENCE: NBE-203-04

CURRENT APPLICATION NUMBER: PCT/US03/10296

CURRENT FILING DATE: 2003-04-04

PRIOR PILING DATE: 2002-04-15

PRIOR PLING DATE: 2002-04-15

PRIOR PLING DATE: 2002-04-15

PRIOR PLING DATE: 2002-04-15

PRIOR PLING DATE: 2002-04-15

SPROR PLING DATE: 2002-04-15

SPROR APPLICATION NUMBER: US 60/421,010

PRIOR APPLICATION NUMBER: US 60/421,010

SPROR APPLING DATE: 2002-04-15

SOFTWARE: Patentin version 3.2

LENGTH: 12
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Sequence 20, Application US/10407637

GENERAL INFORMATION: Methods And Compositions For DNA Manipulation FILE REPERENCE: NEB-203-US

CURRENT APPLICATION NUMBER: US/10/407,637

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 60/372,352

PRIOR APPLICATION NUMBER: US 60/372,675

PRIOR APPLICATION NUMBER: US 60/372,675

PRIOR APPLICATION NUMBER: US 60/421,010

PRIOR PELING DATE: 2002-04-12

PRIOR PELING DATE: 2002-04-12

PRIOR PELING DATE: 2002-04-12

PRIOR RELING DATE: 2002-04-12

PRIOR RELING DATE: 2002-04-12

SPROR FILING DATE: 2002-04-12
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Pred. No. 82;
                   FILE REFERENCE: 47487
CURRENT PEPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 34441
LENGTH: 16
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PCT-US03-10296-20
USES THEREOF
                                                                                                                                                                                                                                                                                                                  38.6%;
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Best Local Similarity 85.7
Matches 12; Conservative
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US-10-310-188-3441
TITLE OF INVENTION:
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ORGANISM: unknown
FEATURE:
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. LOCATION: (1267742) ...(1267757)
. OCHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 507
. PCT-US02-25942-4864
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; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 2219
PCT-US02-25940-18950
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PCT-USO2-5581/C
FCT-USO2-5581, Application PC/TUSO225942
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Sinorhizobium mellioti complete genome, plasmid pS
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION UNMERR: PCT/USO2/25942
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 15792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-USO2-25942-4864/c
| GENERAL INFORMATION: Sequence 4864, Application PC/TUS0225942
| GENERAL INFORMATION: Sinchard J.; Global Determinants, Inc. APPLICANT: Peldmann, Richard J.; Global Determinants, Inc. APPLICANT: Peldmann, Richard J.; Global Determinants, Inc. APPLICANT: Peldmann, Richard J.; Global Determinants, Inc. APPLICATION: Sincrhizobium meliloti complete genome, plasmid pS; FILE REPERBURS: Jm ZOGGEO 103-684-8333
| CURRENT APPLICATION NUMBER: 2002-08-27 CURRENT FILING DATE: 2002-08-27 NUMBER OF SEQ ID NOS: 15792
| NUMBER OF SEQ ID NOS: 15792 | SOGTUMARE: Proprietary SEQ ID NO 4864 | LENGTH: 15
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Sequence 18950, Application PC/TUS0225940

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Delinococcus radiodurans R1 complete genome
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25940

CURRENT FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 25502

SOFTWARE: Proprietary

SEQ ID NO 19950

LENGTH: 15
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ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmi
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Pred. No. 82;
0; Mismatches
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Pred. No. 82;
0; Mismatches
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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Best Local Similarity 91.7
Matches 11; Conservative
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17 AGGGAGTCCAGG 28
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Pred. No. 82;
0; Mismatches 1; Indels
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; Sequence 7, Application PC/TUS0147434
; GENERAL INFORMATION:
APPLICANT: Genaissance Pharmaceuticals, Inc.
APPLICANT: Sanchis, Angela
APPLICANT: Sanchis, Angela
TITLE OF INVENTION: HAPLOTYPES OF THE GPR6 GENE
FILE REFERENCE: GPR6 MWH-1648PCT
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,168
PRIOR PELING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 21
; SGFTWARE PATENTIN OS: 21
; SGFTWARE PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anastasio, Alison E
APPLICANT: Chew, Anne
APPLICANT: Chew, Anne
APPLICANT: Chew, Anne
APPLICANT: Kazemi, Amir
APPLICANT: Kliem, Stefanie E
APPLICANT: Kumar, Annat Madan
APPLICANT: Kumar, Annat Madan
APPLICANT: Kumar, Annat Madan
APPLICANT: Rumar, Annat Madan
APPLICANT: Rumar, Annat Madan
APPLICANT: Parks, Katle B
TITLE OF INVENTION: HAPLOGYPES OF THE MIHFR GENE
FILE REPERENCE: WHIPR MWHIO77-PCT
CURRENT APPLICATION NUMBER: PCT/US01/26488
                                                  DB 1;
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Pred. No. 82;
1; Mismatches
                                                                                             1; Mismatches
                                                Score 10.4;
Pred. No. 82;
                                                                                                                                                                                                                                                                                                             Sequence 60, Application PC/TUS0126488
GENERAL INFORMATION:
APPLICANT: Genalssance Pharmaceuticals, Inc.
APPLICANT: Anastasio, Alison E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227,757
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
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Best Local Similarity 91.7%;
Matches 11; Conservative
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78.6%;
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                                                                                                  Conservative
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PCT-US01-47434-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                         Local Similarity
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       PCT-US01-26215-16
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Best Local Si
Matches 11
                                                Query Match
Best Local 5
                                                                                                  Matches
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: LOCATION: (3645015)...(3645029)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3983
PCT-US02-25943-37161
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OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 5192
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GENERAL INFORMATION:
PAPPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Peeudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25943
CURRENT APPLICATION NUMBER: PCT/US02/25943
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 48484
LENGTH: 15
                                                                                                                                                                         APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PAO1, complete genome.
TITLE OF INVENTION: Pseudomonas aeruginosa PAO1, complete genome.
FILE REPERBNCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PC1/US02/25943
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 3161
LENGTH: 15
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Sequence 62741, Application PC/TUS0225943

Sequence 62741, Application PC/TUS0225943

SEQUENCE 62741, Application PC/TUS0225943

TYPLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.

TITLE REFERENCE: Jim Zegeer Law Offices - 703-684-8333

CURRENT APPLICATION NUMBER: PCT/US02/25943

CURRENT FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 64158

SOFTWARE: Proprietary
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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91.7%; Pred. No. 82;
tive 0; Mismatches
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; Sequence 37161, Application PC/TUS0225943
; GENERAL INFORMATION:
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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nes 11; Conservative
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15 CAGGTAGTCCAG
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; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 37319
PCT-US02-25943-34828
                                                                                                                                 FEATURE: (2239343)...(2239357)

DOTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384 PCT-US02-225943-22682
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Sequence 34828, Application PC/TUSO225943

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REPRENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/USO2/25943

CURRENT FILIND DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 64158

SEQ ID NO 34828

LENGTH: 15
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Sequence 22682, Application PC/TUS0225943
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25943
CURRENT FILING DAIE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 22682
LENGTH: 15
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                                                                TYPE: DNA ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
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Pred. No. 82;
0; Mismatches 1; Indels
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conservative
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Best Local Similarity
  SOFTWARE: Proprietary
                   SEQ ID NO 6581
LENGTH: 15
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SEQ ID NO 62741

15 CAGGTAGTCCAG 4

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Strand = positive ConnectronObjectNumber = 3982
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; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3731
US-10-227-565-34828
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GENERAL INFORMATION:
APPLICAT'S Feldmann, Richard J.; Global Determinants, Inc.
APPLICAT'S Feldmann, Richard J.; Global Determinants, Inc.
ITILE OF INVENTION: Peedwoons aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SCOTWARE Proprietary
SEQ ID NO 37161
LENGTH: 15
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| Sequence 48484, Application US/10227565
| GENERAL INFORMATION:
| APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
| TILLE OF INVENTION: Pseudomonas acruginosa PAO1, complete genome.
| FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
| CURRENT APPLICATION UNBER: US/10/227,565
| CURRENT PILING DATE: 2002-08-26
| NUMBER OF SEQ ID NOS: 64158
| SOFTWARR: Progrietary
| SEQ ID NO 48484
                                            RESULT 158
US-10-227-565-34828/C
US-10-227-565
US-10-227-565
Sequence 34828, Application US/10227565
GENERAL INFORMATION:
SAPLICANT Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PAO1, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PELLING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE PROPRIETATY
SEQ ID NO 34828
LENGTH: 15
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome
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Pred. No. 82;
0; Mismatches
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OTHER INFORMATION: Chromosome = 1
US-10-227-565-37161
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11, Conservative
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384
US-10-227-565-22682
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): OCHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 22195
US-10-227-563-18950
                                                                      FEATURE: (6120631)...(6120645)

OCHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 67218
PCT-US02-25943-62741
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TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,563
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 19950
LENGTH: 15
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GENERAL INFORMATION:
APPLICATURY: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Peeudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-694-8333
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SSQ ID NOS: 64158
SSQ ID NO 22682
LENGTH: 15
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ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmi
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Pred. No. 82;
0; Mismatches 1; Indels
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LENGTH: 15
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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37.1%; Score 10.4; E
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches
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Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches
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; Sequence 18950, Application US/10227563
; GENERAL INFORMATION:
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91.7%;
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Matches 11; Conserv
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LENGTH: 15

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; OTHER INFORMATION: Chromosome = 3 Strand = negative ConnectronObjectNumber = 200!
US-10-227-567-6581
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GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid pS FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION WUMBER: US/10/367,729A
UNMBER OF SEQ ID NOS: 15792
SOFTWARE: Proprietary
SEQ ID NO 85: 15792
LENGTH: 15
                                                            'Sequence 6581, Application US/10227567
'GENERAL INFORMATION:
'GENERAL INFORMATION:
'RAPLICATUR: Feldmann, Richard J.; Global Determinants, Inc.
'RAPLICATUR: Feldmann, Sinorhizobium mellioti complete genome, plasmid pS;
'TITLE OF INVENTION: Sinorhizobium mellioti complete genome, plasmid pS;
'FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
'CURRENT APPLICATION NUMBER: US/10/227,567
'CURRENT PILING DATE: 2002-08-16
'NUMBER OF SEQ ID NOS: 15792
'SOFTWARE: Proprietary
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APPLICATY Feldmann. Richard J., Global Determinants, Inc., TITLE OF INVENTION: Caulobacter crescentus complete genome; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333, CURRENT FILING DATE: 2003-03-03, NUMBER OF SEQ ID NOS: 27958, SEQ ID NOS: 27958; SEQ ID NO 27958; LENGTH: 15
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Pred. No. 82;
0; Mismatches
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; CTHER INFORMATION: Chromosome = 1
US-10-287-787-27958
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: LOCATION: (3538798)...(3538798)
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-367-729A-4864/c
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                                                                                                                                                                                                                                                                                           SEQ ID NO 6581
LENGTH: 15
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1 LOCATION: (6120631)...(6120645)
2 COTER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 67218
US-10-227-565-62741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1267742)...(1267757)
OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 5075
                                            FEATURE:

; LOCATION: (4677818)...(4677832)

; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 51923

US-10-227-565-48484
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TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid pS
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,567
CURRENT FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 15792
SOFTWARE: Proprietary
SEQ ID NO 4864
LENGTH: 15
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 62741, Application US/10227565
SEQUENCE 62741, Application US/10227565
SERERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Peeudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,565
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SSC INDAS: Proprietary
SSC ID NO 62741
LENGTH: 15
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
TYPE: DNA ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 82;
0; Mismatches
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GENERAL INFORMATION:
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il Similarity 91.7%;
11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conserv
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US-10-227-567-4864/c
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US-10-227-565-62741
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; LONDON (3645015)...(3645029)
; LOCATION: (3645015)...(3645029)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 398.
US-10-367-832A-37161
                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (3391804) ... (3391817) ... (CHIOMOSOME = 1 Strand = positive ConnectronObjectNumber = 3737 US-10-367-832A-34828
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TITLE OF INVENTION: Pseudomonas aeruginosa PAO1, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 3161
LENGTH: 15
                               Sequence 34828, Application US/10367832A; Sequence 34828, Application US/10367832A; GENERAL INFORMATION:
A PAPPLICANT: Feldmann, Richard J., Global Determinants, Inc.
TITLE OF INVENTION: Pecudomonas aeruginosa PA01, complete genome.; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 34828
LENGTH: 15
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; Sequence 4844, Application US/10367832A
; GENERAL INFORMATION: Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TILLE OF INVENTION: Pseudomonas acruginosa EA01, complete gent
; TILLE REPRENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NOS: 64158
; SEQ ID NOS: 64844
; TYPE: DNA
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 82;
0; Mismatches
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10s-10-367-832A-37161/c
; Sequence 37161, Application US/10367832A
; GENERAL INFORMATION:
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
                            US-10-367-832A-34828/c
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US-10-367-832A-48484
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ORGANISM: Sinorhizobium meliloti complete genome, plasmid pS
FRATURE:
LOCATION: (1267742)...(1267757)
CHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 5075
US-10-367-729A-4864
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OTHER INFORMATION: Chromosome = 3 Strand = negative ConnectronObjectNumber = 20087
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6581, Application US/10367729A
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J., Global Determinants, Inc.
APPLICANT: Feldmann, Richard J., Global Determinants, Inc.
TITLE OF INVENTION: Sinochium meliloti complete genome, plasmid pS FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION WUMBER: US/10/367,729A
CURRENT FILING DATE: 2003-62-19
NUMBER OF SEQ ID NOS: 15792
SOGTWARE: Proprietary
SEQ ID NO 6581
LENGTH: 15
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Pred. No. 82;
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. OTHER INFORMATION: Chromosome = 1 Strand = negative

US-10-367-832A-22682
                                                                                                                                                         DB 1;
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Pred. No. 82;
0; Mismatches
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ilarity 91.7%;
Conservative
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                Local Similarity
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US-10-367-729A-6581/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-367-729A-6581
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Matches 11
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; LOCATION: (3237918)...(3237933)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3554
PCT-USO2-25943-33165
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| Sequence 33166, Application PC/TUS0225943
| Sequence 33166, Application PC/TUS0225943
| GENERAL INFORMATION:
| APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
| APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
| TITLE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
| CURRENT APPLICATION NUMBER: PCT/US02/25943
| CURRENT FILING DATE: 2002-08-27
| NUMBER OF SEQ ID NOS: 64158
| SEQ ID NO 33166
| LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34829, Application PC/TUS0225943
; Sequence 34829, Application PC/TUS0225943
; GENERAL INFORMATION:
    PAPPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
    TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
    FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICANTION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SEQ ID NO 34829
; LENGTH: 16
                      Sequence 33155, Application PC/TUS0225943
(SEQUENCE 33155, Application PC/TUS0225943
(SENERAL INFORMATION:
APPLICAT'S Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Peedudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
(CURRENT PELLING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 33165
LENGTH: 16
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 95;
0; Mismatches
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Matches 11, Conservative
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PCT-US02-25943-34829
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Best Local
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| OCTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 22195
| US-10-367-892-18950
                      ; LOCATION: (4677818)...(4677832)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 51923
US-10-367-832A-48484
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GENERAL INFORMATION.
APPLICANT: Feldmain. Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, FILE REFRENCE: Jim Zeger. Law Offices - 703-684-8333
CURRENT APPLICATION WUMBER. US/10/367,892
CURRENT FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 18950
LENGTH: 15
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
ORGANISM: Pseudomonas aeruginosa PA01, complete genome
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Pred. No. 82;
0; Mismatches 1;
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Pred. No. 82;
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Best Local Similarity 91.7%;
Matches 11; Conservative C
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91.7%;
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Best Local Similarity
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US-10-367-892-18950/c
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; IOCATION: (3391804)...(3391818)
; OCHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3732
US-10-227-565-34829
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  Sequence 34829, Application US/10227565
; Sequence 34829, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Peeudomonas aeruginosa PA01, complete genome.
; TITLE OF INVENTION: Peeudomonas aeruginosa PA01, complete genome.
; CURRENT PEPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SEQ ID NO 34829
; LENGTH: 16
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US-10-305-274-1406
US-10-305-274-1406
US-10-305-274-1406
US-10-305-274-1406
SEQUENCE 1406, Application US/10305274
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.; TTLLE OF INVEXTION: Aguifex aeolicus complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/305,274
CURRENT FILING DATE: 2002-11-27
NUMBER OF SEQ ID NOS: 1550
; SOFURARE: Proprietary
; SEQ ID NO 1406
; LENGTH: 16
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Sequence 517, Application US/10305274
GENERAL INFORMATION:
GENERAL INFORMATION:
TTILE OF INVENTION: Aquifex aeolicus complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/305,274
CURRENT FILING DATE: 2002-11-27
NUMBER OF SEQ ID NOS: 1550
SOFTWARE: Proprietary
SEQ ID NO 517
LENGTH: 16
                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 95;
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Pred. No. 95;
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ORGANISM: Aquifex aeolicus complete genome.
PEATURE:
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; OTHER INFORMATION: Chromosome = 1
US-10-305-274-517
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91.7%;
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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Best Local Similarity 91.,
Best Local 11, Conservative
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3555¢
US-10-227-565-33166
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1. LOCATION: (3237918)...(3237933)
2. OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 35549
US-10-227-565-33165
FEATURE:
1 LOCATION: (3391804)...(3391818)
2 OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 37320
PCT-US02-25943-34829
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GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OP INVENTION: Desudomonas aeruginosa PAD1, complete genome.
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,565
NUMBER OF SEQ ID NOS: 64158
SOFTWARE Proprietary
SEQ ID NO 33166
LENGTH: 16
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TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,565
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SSCPTWARE: Proprietary
SEQ ID NO 31165
LENGTH: 16
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Best Local Similarity 91.7%; Pred. No. 95;

Matches 11; Conservative 0; Mismatches 1; Indels
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome
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Pred. No. 95;
0; Mismatches
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Pred. No. 95;
0; Mismatches
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7%;
Matches 11; Conservative
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16 CAGGTAGTCCAG 5
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US-10-227-565-33165/c
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; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 145(
PCT-US02-25940-12401
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PCT-USO2-25940-14568
PCT-USO2-25940-14568. Application PC/TUSO225940
SEQUENCE 14568. Application PC/TUSO25940
GENERAL INFORMATION:
TITLE OF INVENTION: Delinococcus radiodurans R1 complete genome, Plasmi; TITLE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/USO2/25940
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 25502
SOCTOR PROPRIET PROPRIETARY
SEQ ID NO 14568
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Sequence 34829, Application US/10367832A
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Desudomonas aeruginosa PAO1, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SSQ ID NO 34829
LENGTH: 16
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GENERAL INFORMATION:
APPLICANT: Feldmann. Richard J.; Global Determinants, Inc.:
TITLE OF INVENTION: Delinococcus radiodurans R1 complete ge;
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 12401
LENGTH: 15
                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 95;
0; Mismatches
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80.0%; Pred. No. 88;
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US-10-367-832A-34829
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 12, Conservative
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PCT-US02-25940-12401
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/ OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 35550 US-10-367-812A-33166
       ; LOCATION: (1394218)...(1394232)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1909
US-10-305-274-1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (3237918)...(3237933)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 35549
US-10-367-832A-33165
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENDMENT, Feldmenn, Richard J.; Global Determinants, Inc.
TITLE OF INVENTUON: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PRILIG DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 33166
LENGTH: 16
                                                                                                                                                                                                                                                                                                         RESULT 181
US-10-367-83165/A
US-10-367-832A-33165/C
Sequence 33165, Application US/10367832A
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION:
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICAND NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 33165
LENGTH: 16
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 95;
0; Mismatches
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Pred. No. 95;
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91.7%;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11, Conservative
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Matches 11, Conservative
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US-10-367-832A-33166
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US-10-367-832A-34829
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LOCATION: (3030196)...(3030210)

CHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3336
PCT-US02-25943-31163
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1 LOCATION: (3020196)...(3030210)
2 COTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3336
PCT-US02-25943-31162
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Sequence 897, Application US/09406643

Sequence 897, Application US/09406643

APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ludwig, Janos

APPLICANT: Lebende

TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
FILE REFERENCE: MBH800-874-A (237/197)

CURRENT APPLICATION NUMBER: US/09/406,643

CURRENT PILING DATE: 1999-09-27

PRIOR APPLICATION NUMBER: US 08/879,078

PRIOR FILING DATE: 1997-06-19

PRIOR FILING DATE: 1997-06-19

NUMBER OF SEQ ID NOS: 2606

SOFTWARE: PatentIn version 3.0
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PCT-USO2-25943-31163/c

Sequence 31163, Application PC/TUSO225943

GENERAL INFORMATION:

APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

TITLE OF INVENTION: Resendencias aeruginosa PAO1, complete genome.

FILE REPRENCE: Jim Zegeer Law Offices - 703-684-8333

CURRENT APPLICATION NUMBER: PCT/USO2/25943

CURRENT FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 64158

SEQ ID NO 31163

LENGTH 15
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        APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PAO1, complete genome.
FILE REPERBNES. Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION WUBBER: PCT/USO2/25943
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 31162
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome
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36.4%; Score 10.2; D
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches
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Best Local Similarity
  GENERAL INFORMATION:
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US-09-406-643-897/c
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1 LOCATION: (2698124)...(2698138)

OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 29757

PCT-US02-25943-27773
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 17012 PCT-US02-25940-14568
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Sequence 6183, Application PC/TUSO255943
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/USO2/25943
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 6183
LENGTH: 15
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Pred. No. 88;
0; Mismatches 3; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
SEPLICATION:
FILE REPRINCE: Jim Zeger Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-08-77
NUMBER OF SEQ ID NOS: 64158
SEQ ID NOS: 64158
SEQ ID NO 27773
LENGTH: 15
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 88;
0; Mismatches
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PCT-US02-25943-31162/c
; Sequence 31162, Application PC/TUS0225943
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| OTHER INFORMATION: Chromosome = 1
| PCT-US02-25943-6183
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80.0%;
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Best Local Similarity 80.0%;
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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     0; Mismatches
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, OTHER INFORMATION: P(qs)1 DNA probe
US-09-912-673A-55
                                                                                                                                                                                                                  US-09-879-813-73/c
; Sequence 73, Application US/09879813
; GENERAL INFORMATION:
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Best Local Similarity 80.0%;
Matches 12; Conservative
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     12; Conservative
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     Matches
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APPLICANT: Koshy, Beena
APPLICANT: Koshy, Beena
APPLICANT: Koshy, Beena
APPLICANT: Genaiseance Pharmaceuticals
APPLICANT: Genaiseance Pharmaceuticals
TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the G
TITLE OF INVENTION: Proctein-Coupled Receptor 8 Gene
FILE REFERENCE: MWH-567US
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
IENGTH: 15
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US-09-498-824A-897/C
Sequence 897, Application US/09498824A
GENERAL INFORMATION:
APPLICANT: Riboxyme Pharmaceuticals, Inc.
APPLICANT: Bidoxyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
FILE REFERENCE: MBH800-874-D (447/280)
CURRENT APPLICATION NUMBER: US/09/498,824A
CURRENT FILING DATE: 2000-02-04
FRIOR PLILING DATE: 1997-06-19
FRIOR PLLING DATE: 1997-06-19
FRIOR FILING DATE: 1997-06-19
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                                                                                                                                                           Score 10.2; DB 1;
Pred. No. 88;
0; Mismatches 3;
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80.0%; Pred. No. 88;
tive 0; Mismatches
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Pred. No. 88;
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US-09-611-577-21/c
Sequence 21, Application US/09611577
GENERAL INFORMATION:
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80.0%;
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Best Local Similarity 80.0%;
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-09-611-577-21
; SEQ ID NO 897
; LENGTH: 15
: TYPE: RNA
; ORGANIEM: Homo sapiens
US-09-406-643-897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
CORGANISM: Homo sapiens
US-09-498-824A-897
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Best Local Similarity
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FEATURE:
NAME/KEY: misc\_feature
COCATION: (7)...(10)
GTHER INFORMATION: F264
US-09-879-813-73 .; 0 ö DB 1; Length 15; Score 10.2, DB 1, Length 15; Pred. No. 88; 0; Mismatches 3; Indels Indels RESULT 194
US-09-912-673A-55/c
| Sequence 55, Application US/09912673A|
| GENERAL INFORMATION:
| APPLICANT: Ye, Bangce
| TILLE OF INVENTION: WEDIUM AND LOW DENSITY GENE CHIPS|
| FILE REFERENCE: JNB 100
| CURRENT FILING DATE: 2001-07-23
| NUMBER OF SEQ ID NOS: 70
| SOFTWARET PAILED APPLICATION NUMBER: US/09/912,673A|
| SOFTWARET FILING DATE: 2001-07-23
| SOFTWARET PAILED APPLICATION NUMBER: US/09/912,673A|
| SEQ ID NO 55 APPLICANT: Sale, Julian E.
APPLICANT: Sale, Michael S.
APPLICANT: Neuberger, Michael S.
APPLICANT: Cumbers, Sarah J.
TITLE OF INVENTION: Method of Generating Diversity
FILE REFERENCE: 18396/2005
CURRENT APPLICATION NUMBER: 05/828,717
PRIOR PILING DATE: 2001-06-11
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 73
LENGTH: 15

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LOCATION: (1754821)...(1754835)
CTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1701
US-10-227-563-14568
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LOCATION: (542693)...(542707)
OTHER INORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = US-10-227-565-6183
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                                           JECTURE 14568, Application US/10227563
Sequence 14568, Application US/10227563
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Delinococcus radiodurans R1 complete genome, Plasmi;
TITLE OF INVENTION: Delinococcus radiodurans R2 complete genome, PILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION UNBER: US/10/227,563
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 25502
SOOFWARE: Proprietary
SEQ ID NO 14568
LENGTH: 15
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GENERAL INFORMATION:
APPLICATION:
PAPPLICATION: Redemonas aeruginosa PA01, complete genome.
TITLE OF INVENTION: Peeduconosa aeruginosa PA01, complete genome.
CURRENT APPLICATION NUMBER: US/10/227,565
CURRENT PILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 2773
LENGTH: 15
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; Sequence 6183 Application US/10227565
; GENERAL INFORMATION:
; APPLICANT Feldmann, Richard J.; Global Determinants, Inc.
; TILE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFRENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; NUMBER: OF SEQ ID NOS: 64158
; SOUTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
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36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmi
FEATURE:
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36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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ORGANISM: Pseudomonas aexuginosa PA01, complete genome
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US-10-227-565-27773
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; LOCATION: (1491220)...(1491234)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 14502
US-10-227-563-12401
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GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Deinooccus radiodurans R1 complete genome, Plasmi
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,563
CURRENT FILING DATE: 2502-08-26
NUMBER OF SEQ ID NOS: 25502
SOPTWARE: Proprietary
SEQ ID NO 12401
LENGTH: 15
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ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmi
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              GENERAL INFORMATION:
APPLICANT: Sale, Julian E.
APPLICANT: Sale, Julian E.
APPLICANT: Neuberger, Michael S.
APPLICANT: Cumbers, Sarah J.
TITLE OF INVENTION: Method of Generating Diversity
FILE REFERENCE: 18396/2005B
CURRENT APPLICATION NUMBER: US/10/146,505
CURRENT APPLICATION NUMBER: 09/828,717
PRIOR APPLICATION NUMBER: 09/828,717
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR PRIOR APPLICATION NUMBER: GB 992104.7
PRIOR FILING DATE: 1999-10-09
PRIOR FILING DATE: 1999-10-09
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: GB 9913435.5
PRIOR FILING DATE: 1999-01-19
PRIOR PRILING DATE: 1999-01-19
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ORGANISM: Homo sapiens
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US-10-227-563-12401
US-10-146-505-73/c
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; LOCATION: (2480655)...(2480669)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 181'
US-10-287-787-16396
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                                                                APPLICANT: Feldemain, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Caulobacter crescentus complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,787
CURRENT APPLICATION DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 27958
SOFTWARE: Proprietary
SEQ ID NO 16396
LENGTH: 15
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GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT Feldmann, Richard J.; Global Determinants, Inc.;
TITLE OF INVENTION: Caulobacter crescentus complete genome
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,787

CURRENT FILING DATE: 2003-03,0303-03

NUMBER OF SEQ ID NOS: 27958

SEQ ID NO 16397

LENGTH: 15
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ORGANISM: Caulobacter crescentus complete genome
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Pred. No. 88;
O; Mismatches
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llarity 80.0%; Pred. No. 88;
Conservative 0; Mismatches
       ; Sequence 16396, Application US/10287787; GENERAL INFORMATION:
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US-10-287-787-16397
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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Matches 12; Conserv
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100ATION: (3030196)...(3030210)
100ATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33366
US-10-227-565-31162
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33365
US-10-227-565-31163
LOCATION: (2698124)...(2698138)
CHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 29757
US-10-227-565-27773
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GENERAL INFORMATION: Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Reaudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PELING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SCOTUMAER: Proprietary
SEQ ID NO 31163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASOLID-27-565-31162/c

Sequence 31162, Application US/10227565

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFRENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PRILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158

SOFTWARE: Proprietary
SOFTWARE: Proprietary
LENGTH: 15
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome
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80.0%; Pred. No. 88;
tive 0; Mismatches
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36.4%; Score 10.2; 1
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches
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Best Local Similarity 80.0%;
Matches 12; Conservative
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Matches 12; Conservative
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US-10-227-565-31163/c
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FEATURE:

LOCATION: (2698124)...(2698138)

CTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 297E

US-10-367-832A-27773
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                                                                                                                                                                                                                 | LOCATION: (542693)...(542707)
| OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = US-10-367-832A-6183
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APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TILE OF INVENTION: Pseudomonas aeruginosa PAO1, complete genome.
PILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SEQ ID NOS: 64158
SEQ ID NO 31162
LENGTH: 15
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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                                                                                                                                                       TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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CTHER INFORMATION: Chromosome = 1 Strand = negative US-10-367-832A-31162
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333;
CURRENT APPLICATION NUMBER: US/10/367,832A;
NUMBER OF SEQ ID NOS: 64158;
SOFTWARE: Proprietary
SOFTWARE: Proprietary
SOFTWARE: Proprietary
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Pred. No. 88;
0; Mismatches
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80.0%; Pred. No. 88;
tive 0; Mismatches
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80.0%;
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Best Local Similarity 80.0
Matches 12, Conservative
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Best Local Similarity 80.0
Marches 12; Conservative
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US-10-367-832A-31162/c
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GENERAL INFORMATION:
APPLICANT: ROSettademonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERRNCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 22105
LENGTH: 15
                                                                                                                                                                                                                                                                                                     US-10-130-188-22102
Sequence 22102. Application US/10310188
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN version 3.1
SOFTWARE: PATENTIN version 3.1
                           = 28230
    ; LOCATION: (3679402)...(3679417)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber US-10-287-787-25557
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SEQUENCE INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TILLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
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Pred. No. 88;
0; Mismatches 3;
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Pred. No. 88;
0; Mismatches
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Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 80.0°
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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CORGANISM: Homo sapiens
US-10-310-188-22102
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US-10-310-188-22105
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US-10-310-188-22105
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US-10-367-832A-6183
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ConnectronObjectNumber = 1707
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Sequence 897, Application US/10453850

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Broat, Janos
APPLICANT: Broat, Lecnid
APPLICANT: Bedgelman, Lecnid
ITLE OP INVENTION: Compositions Having RNA Cleaving Activity
FILE REFERENCE: MBH800-874-A (2377187)
CURRENT APPLICATION NUMBER: US/10/453,850
CURRENT APPLICATION NUMBER: US/30/66.43
PRIOR APPLICATION NUMBER: US/80/66.43
PRIOR PILING DATE: 1999-09-27
PRIOR FILING DATE: 1997-06-19
PRIOR FILING DATE: 1997-06-19
PRIOR FILING DATE: 1997-06-19
PRIOR FILING DATE: 1997-06-19
PRIOR FILING DATE: US 08/878,640
PRIOR POLICATION NUMBER: US 08/878,640
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                                                                                                                                       TYPE: DNA
ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmi
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Pred. No. 88;
0; Mismatches
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Pred. No. 88;
    CURRENT APPLICATION NUMBER: US/10/367,892
CURRENT FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 25502
SEGTWARE: Proprietary
SEQ ID NO 14568
LENGTH: 15
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80.0%;
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SOFTWARE: Patentin version 3.0
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Best Local Similarity 80.0°
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-453-850-897
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COTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33365
US-10-367-832A-31163
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COTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 14502

US-10-367-892-12401
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GRNERAL INFORMATION:
APPLICAMY: Feldmann, Richard J.; Global Deferminants, Inc.
TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,892
CURRENT FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 12401
LENGTH: 15
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TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
                                                                                                                                                                                                 165-10-367-832A-31163/c

| Sequence 31163, Application US/10367832A
| GENERAL INFORMATION:
| APPLICANT's Feldmann, Richard J.; Global Determinants, Inc.
| TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
| FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
| CURRENT APPLICATION: DA078: US/10/367,832A
| CURRENT FILING DATE: 2002-08-26
| NUMBER OF SEQ ID NOS: 64158
| SOFTWARE: Proprietary
| SEQ ID NO 31163
| LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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Best Local Similarity 80.0%; Pred. No. 88; Matches 12; Conservative 0; Mismatches
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Pred. No. 88;
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80.0%; Pred. No. 88;
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; Sequence 14568, Application US/10367892
; GENERAL INFORMATION:
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80.0%;
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Matches 12; Conserv
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April 19, 2004, 15:06:48; Search time 0.001 Seconds (without alignments) 116.984 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on:

US-10-024-396-3-COPY 28 Title: Perfect score:

28

1 cgggccctacgtgtacagggagtccagg Sequence:

IDENTITY NUC Gapoxt 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

180 seqs, 2089 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 218 summaries

issab: Issued-Patents-NA Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 19, Appli Sequence 6, Appli Sequence 18, Appli Sequence 18, Appl Sequence 18, Appl Sequence 129, Appl Sequence 6, Appli Sequence 6, Appli Description Sequence 2 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence SUMMARIES Query Match Length DB U

quence 11E quence 23, quence 2, quence 2, quence 67, quence 20, quence 20, quence 20, quence 20, quence 20, quence 21, quence 21,	diquence 85, diquence 85, diquence 85, diquence 86, diquence 86, diquence 86, diquence 25, dique	equence 19 equence 20 equence 24 equence 24 equence 12 equence 12 equence 12 equence 19 equence 9, equence 17 equence 17 equence 17 equence 17 equence 17 equence 17	orento composition of the control of
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8-551B-657 8-551B-658 8-551B-661 8-551B-661 8-551B-813 8-551B-814 8-561B-814	1. 178. 1830 Sequence Sequence 3-789-1631 Sequence 3-789-1631 Sequence 3-555. 5-55 Sequence 3-555. 5-55 Sequence 3-555. 5-55 Sequence 3-555. 155. 155. 155. 155. 155. 155. 155.	11-1378-37 Sequence 89-804A-37 Sequence 86-85A-3 Sequence 89-7693-37 Sequence 89-789-2122 Sequence 89-789-2122 Sequence 89-789-2331 Sequence 89-789-2347 Sequence 89-789-2347 Sequence 89-789-2348 Sequence 89-789-2348 Sequence 85-80-190-19 Sequence 85-80-190-19 Sequence 85-80-190-19 Sequence 85-80-190-19 Sequence 88-85-86-190-19 Sequence 88-85-86-190-190-191-190-191-190-191-190-191-191
1 US-08-488-5518-655 Sequence 1 US-08-488-5518-656 Sequence 1 US-08-488-5518-661 Sequence 1 US-08-488-5518-813 Sequence 1 US-08-488-5518-813 Sequence 1 US-08-488-5518-814 Sequence 1 US-09-425-738-12 Sequence 1 US-09-425-738-17 Sequence 1 US-09-462-5618-26 Sequence 1 US-09-462-5618-26 Sequence 1 US-09-462-5618-26 Sequence 1 US-09-462-181 Sequence 1 US-09-462-181 Sequence 1 US-09-462-181 Sequence 1 US-09-462-181 Sequence 1 US-09-462-181 Sequence 1 US-09-462-181 Sequence 1 US-09-761-132-10 Sequence	1 US-09-989-789-1631 Sequence 1 US-07-981-789-1631 Sequence 1 US-08-459-448-55 Sequence 1 US-08-459-444-55 Sequence 1 US-09-249-155A-29 Sequence 1 US-09-249-155A-29 Sequence 1 US-09-249-155A-31 Sequence 1 US-09-249-155A-31 Sequence 1 US-09-249-155A-31 Sequence 1 US-09-249-155A-35 Sequence 1 US-08-327-525A-35 Sequence 1 US-08-327-525A-35 Sequence 1 US-09-281-418-25 Sequence 1 US-09-281-418-25 Sequence 2 US-08-859-954-297 Sequence 1 US-08-859-954-297 Sequence 1 US-08-859-954-436 Sequence 1 US-08-859-954-437 Sequence 1 US-08-859-954-437 Sequence 1 US-08-859-954-437 Sequence 1 US-08-859-954-437 Sequence 1 US-08-819-954-31 Sequence	1 US-08-331 Sequence 1 US-08-759-804A-37 Sequence 1 US-09-046-858A-3 Sequence 1 US-09-266-8537 Sequence 1 US-09-289-789-2121 Sequence 1 US-09-989-789-2122 Sequence 1 US-09-989-789-2331 Sequence 1 US-09-989-789-2331 Sequence 1 US-09-989-789-2347 Sequence 1 US-09-989-789-2347 Sequence 1 US-09-989-789-2347 Sequence 1 US-09-989-789-2348 Sequence 1 US-09-450-515-3 1 US-09-450-515-3 1 US-08-288-19 Sequence 1 US-09-785-716A-18 Sequence 1 US-09-785-716A-18 Sequence 1 US-08-588-19 Sequence 1 US-08-488-5518-659 Sequence
10 1 US-08-488-551B-656 Sequence 10 1 US-08-488-551B-656 Sequence 10 1 US-08-488-551B-651 Sequence 10 1 US-08-488-551B-661 Sequence 10 1 US-08-488-551B-813 Sequence 10 1 US-08-488-551B-813 Sequence 10 1 US-09-425-798-12 Sequence 10 1 US-09-425-798-12 Sequence 10 1 US-09-462-561B-26 Sequence 10 1 US-09-462-561B-26 Sequence 10 1 US-09-303-153B-160 Sequence 10 1 US-09-769-482-18 Sequence 10 1 US-09-769-183-163 Sequence 10 US-09-183-183-183-183-183-183-183-183-183-183	10 1 US-09-989-789-16310 Sequence 10 1 US-09-989-789-16310 Sequence 11 1 US-09-989-789-16310 Sequence 11 1 US-09-989-789-1631 Sequence 11 1 US-08-459-5548-55 Sequence 11 1 US-08-459-5048-55 Sequence 11 1 US-08-459-648-55 Sequence 11 1 US-09-153-242-29 Sequence 11 1 US-09-153-242-29 Sequence 11 1 US-09-153-242-29 Sequence 11 1 US-09-153-243-162 Sequence 11 1 US-09-153-153A-162 Sequence 11 1 US-09-154-155A-231 Sequence 11 1 US-09-158-76-35 Sequence 11 1 US-09-158-76-35 Sequence 12 US-08-158-76-35 Sequence 12 US-08-158-76-35 Sequence 12 US-08-158-76-35 Sequence 12 US-08-158-76-35 Sequence 13 US-08-158-76-35 Sequence 14 US-08-158-76-35 Sequence 15 US-08-158-954-179 Sequence 16 US-08-158-954-179 Sequence 18 US-08-158-954-137 Sequence 18 US	9 1 US-08-31-3978-37 Sequence Construction of the Construction of
26.4 10 1 US-08-488-551B-656 Sequence 26.4 10 1 US-08-488-551B-656 Sequence 26.4 10 1 US-08-488-551B-656 Sequence 26.4 10 1 US-08-488-551B-661 Sequence 26.4 10 1 US-08-488-551B-814 Sequence 26.4 10 1 US-08-488-551B-814 Sequence 26.4 10 1 US-09-425-798-12 Sequence 26.4 10 1 US-09-425-798-12 Sequence 26.4 10 1 US-09-462-561B-26 Sequence 26.4 10 1 US-09-462-561B-26 Sequence 26.4 10 1 US-09-462-561B-16 Sequence 26.4 10 1 US-09-462-561B-16 Sequence 26.4 10 1 US-09-482-18 Sequence 26.4 10 1 US-09-482-18 Sequence 26.4 10 1 US-09-482-18 Sequence 26.4 10 1 US-09-5482-18 Sequence 26.4 10 1 US-09-5	26.4 10 1 US-09-389-789-1631 Sequence 26.4 11 1 US-09-987-789-1631 Sequence 26.4 11 1 US-09-987-789-1631 Sequence 26.4 11 1 US-08-459-5948-55 Sequence 26.4 11 1 US-08-459-6448-55 Sequence 26.4 11 1 US-08-459-444-55 Sequence 26.4 11 1 US-08-459-444-55 Sequence 26.4 11 1 US-09-54-1554-61 Sequence 26.4 11 1 US-09-54-1554-61 Sequence 26.4 11 1 US-09-54-1554-61 Sequence 26.4 11 1 US-09-549-1554-35 Sequence 26.4 11 1 US-09-549-1554-35 Sequence 25.7 11 1 US-09-549-1554-35 Sequence 25.7 11 1 US-09-511-1379-35 Sequence 25.7 11 1 US-09-281-418-25 Sequence 25.7 11 1 US-09-281-418-25 Sequence 25.7 11 1 US-09-281-418-25 Sequence 25.7 12 1 US-09-281-418-25 Sequence 25.7 12 1 US-09-581-418-25 Sequence 25.7 12 US-09-581-418-25 Sequence 25.7 12 US-08-859-954-37 Sequence 25.0 8 1 US-08-954-37 Sequence 25.0 8 1 US-08-954-31 Sequence 25.0 8 1 US-08-959-954-31 Sequence 25.0 8 1 US-08-959-954-31 Sequence 25.0 8 1 US-08-859-954-31 Sequence 25.0 8 1 US-08-859-954-31 Sequence 25.0 8 1 US-08-959-954-31 Sequence 25.0 8 1 US-08-859-954-31 S	25.0 9 1 US-0B-31.397B-37 Sequence 25.0 9 1 US-0B-31.397B-37 Sequence 25.0 9 1 US-0B-046-858A-3 Sequence 25.0 9 1 US-0B-046-858A-3 Sequence 25.0 9 1 US-09-989-789-2122 Sequence 25.0 9 1 US-09-989-789-2122 Sequence 25.0 9 1 US-09-989-789-2131 Sequence 25.0 9 1 US-09-989-789-2331 Sequence 25.0 10 US-09-989-789-234 Sequence 25.0 10 US-09-989-789-234 Sequence 25.0 10 US-09-785-716A-18 Sequence 25.0 10 US-08-988-19 Sequence 25.0 10 US-08-988-19 Sequence 25.0 10 US-08-988-19 Sequence 25.0 10 US-08-988-19 Sequence 25.0 10 US-08-988-185-659 Sequence 25.0 10 US-08-988-5118-659 S
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USEGUENT BATTATA-6/C

SEQUENCE 6, Application US/09075717A

PATER NO. 6174869

PATER NO. 6174869

PATER NO. 6174869

TITLE OF INVENTION: AND AGENTS USEFUL FOR SAME
NUMBER OF SEQUENCES:
STREET: 400 Garden City Plaza
COURTR: US.A.

COURTR: US.A.

COURTR: US.A.

CONFIRE: New York
COUNTR: US.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: BLEENITH Release #1.0, Version #1.30

COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPS/MS-DOS

SOFTWARE BATTION DATA:
APPLICATION NUMBER: US/09/075,717A

FILING DATE: UJ-UJ-1996
APPLICATION NUMBER: 18 40 M/1870
FILING DATE: US-UJ-1996
APPLICATION NUMBER: 13.346
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.9%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 4.5; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08630592
Patent No. 5770432
CENERAL INPORMATION
APPLICANT: Nishina, Patey
APPLICANT: No. 5770432enTrauth, Konrad
APPLICANT: No. 5770432th, Michael
TILE OF INVENTION: Obesity Associated Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 TGTACAGGGAGTCCA 26
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-630-592-18
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| Sequence 6, Application US/08633792A
| Patent No. 5837594
| GENERAL INFORMATION: A METHOD FOR ENHANCING NEURONE SURVIVAL
| TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
| TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
| TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURING SOLING, SOCIETY (OR SAME NUMBER OF SEQUENCES: 9
| CORRESPONDENCE ADDRESS: 9
| CORRESPONDENCE ADDRESS: 9
| CORPTER: OR SECUENCES: 9
| COMPTER: NEADABLE FORM: NEW YORK COUNTRY: U.S.A. (ITY)
| COMPTER: TEADABLE FORM: NEOROWING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTION NUMBER: US/08/633,792A |
| CORPTER: OR PEDICATION NUMBER: US/08/633,792A |
| CORPTER: OR PEDICATION NUMBER: US/08/633,792A |
| CLASSIFICATION NUMBER: US/08/633,792A |
| PRIOR APPLICATION NUMBER: US/08/633,792A |
| TELECOMMUNICATION NUMBER: 13/36 |
| REFERENCE CHARACTERISTICS: US/08/142-4343 |
| TELECOMMUNICATION NUMBER: 13/36 |
| REPERENCE OF AND STAINS UR |
| NUMBER: US/08/64 |
| TELECOMMUNICATION NUMBER: US/08/64 |
| TELECOMUNICATION NUMBER: US/08/64 |
| TOPOLOGY: LINEAR |
| NOBLECULE TYPE: UNCIDENCE CHARACTERISTICS: US/08/64 |
| TOPOLOGY: LINEAR |
| NOBLECULE TYPE: UNCIDENCE CHARACTERISTICS: US/08/64 |
| TOPOLOGY: UNDER US/08/64 |
| MOLECULE TYPE: UNCIDENCE US/08/64 |
| TOPOLOGY: UNDER US/08/64 |
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47.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.5;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.7%; Score 14.2; DB 1; Length 21; Best Local Similarity 84.2%; Pred. No. 3.7; Matches 16; Conservative 0; Mismatches 3; Indels
| TELEPHONE: (516) 742-4343
| TELERAX: (516) 742-4366
| TELEX: 203 901 SANS UR
| TELEX: 203 901 SANS UR
| INFORMATION FOR SEQ ID NO: 19:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 21 base pairs
| TYPE: nucleic acid
| STRANDENNESS: single
| TOPOLOGY: linear:
| MOLECULE TYPE: DNA (genomic)
| US-08-702-665A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CGTGTACAGGGAGTCCAGG 28
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Gaps

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Length 19;
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195-09-02-365A-30

Sequence 30, Application US/09032365A

Patent No. 6114502

GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: Nishina, Patsy
APPLICANT: No. 6114502en-Trauth, Konrad
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
TITLE OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, Lip
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
CONUTRY: USA
ZIP: 34301
COMPUTER READALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SESSEE OF Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
FRING BATE:
FILING BATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

44.3%; Score 12.4; D

Best Local Similarity 92.9%; Pred. No. 10;

Matches 13; Conservative 0; Mismatches
                                                TELEX: 910 277299;
information FOR SEQ ID No: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: Linear
MICHOLOGY: Linear
MICHOLOGY: Linear
DESCRIPTION: /desc = "primer"
US-08-714-991-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Shewrood, Pamela J.
REGISTRATION NUMBER: 35,677
REFERENCE/DOCKET NUMBER: SEQ-
TELECOMMINICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEPAX: 650-327-3231
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | INPORMATION FOR SEQ ID NO: 3
| SEQUENCE CHARACTER.STICS:
| LENGTH: 19 base pairs
| TYPE: nucleic acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 ACAGGGAGTCCAGG 28
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Best Local Similarity
Matches 13; Conserva
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Sequence 18, Application US/08714991

Patent No. 5776762

GENERAL INFORMATION:

APPLICANT: NORTH, Michael

APPLICANT: NOSTRINA, Patsy

APPLICANT: No. 5776762en-Trauth, Konrad

APPLICANT: NOSTRINA, Denegan

ITILE OF INVENTION: OBESITY ASSOCIATED GENES

NORRESPONDENCE 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STRATE: California

COUNTRY: USA

IP 4111-4187

COMPUTER: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICANION NUMBER: US/08/714,991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 19;
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                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Telopy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PCDOS/MSOOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,592
FILING DATE:
CLASSIFICATION NUMBER: US/08/630,592
ATTORNEY/AGENT INFORMATION:
NAMB: SCHAWOOO, PEMGLA J.
REGISTRATION NUMBER: A59504/BIR/PJS
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 3983249
TELEPRAX: (416) 3983249
TELEPR
: 3400 Embarcadero Center, Suite 3400
San Francisco
California
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.3%; Score 12.4; D
92.9%; Pred. No. 10;
tive 0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: SFERMOOD, Pamela J.
REGISTATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-59:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 ACAGGGAGTCCAGG 28
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Best Local Similarity 92.9
Matches 13; Conservative
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Gaps

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Sequence 129, Application US/08117952

| Sequence 129, Application US/08117952
| Patent No. 585176
| Patent No. 585176
| Patent No. 585176
| APPLICANT: Enith, Michael W. SAMPLED WARS OF COMPLEX GENOMES
| OORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ADDRE

TOPOLOGY: linear MOLECULE TYPE: Oligonucleotide

; ANTI-SENSE: NO US-08-117-952-129

DB 1; Length 18; 3; Indels Query Match
Best Local Similarity 82.4%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches

Gaps

11 GTGTACAGGGAGTCCAG 27

US-08-970-269A-6

Sequence 6, Application US/08970269A
Patent No. 5976803
GENERAL INFORMATION:
APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES:
ADDRESSE: Dr. Benjamin A. Adler

DB 1; Length 18; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
COMPUTER: Apple
COMPUTER: Apple
CORRATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970.269A
FILING DATE: No. 5976803ember 14, 1997
CIASASIFFCATION:
NAME: Adler Ph.D., Benjamin A.
REGASTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-6908
INFORMATION FOR SEQ ID NO: 6:
SEMENTION FOR SEQ ID NO: 6: TYPE: nucleic acid STRANDEDNESS: double stranded TOPOLOGY: linear MOLECULE TYPE: DESCRIPTION: other nucleic acid HYPOTHETICAL: no 8011 Candle Lane STREET: 8011 Carry: Houston STATE: Texas COUNTRY: US

3; Indels 43.6%; Score 12.2; Di 82.4%; Pred. No. 10; tive 0; Mismatches Query Match
Best Local Similarity 82.4<sup>1</sup>
Matches 14; Conservative

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US-09-407-562-6

1 Sequence (Application US/09407562)

Patent No. 6294334

GENERAL INPORMATION:

APPLICANT: Ratheryn Meek

TITLE OF INVENTION: Genetic Test For Equine Severe

TITLE OF INVENTION: Genetic Test For Equine Severe

TITLE OF INVENTION: Genetic Test For Equine Severe

TITLE OF INVENTION: Condined Immunodeficiency Disease

NUMBER OF SEGUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSER: Dr. Benjamin A. Adler

STREET: 8011 Candle Lane

CITY: Housencon

STREET: Texas

COUNTRY: USA

ZIP: 77071

COMPUTER: Apple

COMPUTER: Apple

OPERATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word for Macintosh

SOFTWARE: Microsoft Word for Macintosh

CURRENT APPLICATION DATA:

PRIOR APPLICATION

PRIOR APPLICATION

APPLICATION

APPLICATION

APPLICATION

TIME DATE:

CLASSIFICATION:

FILING DATE:

PRIOR APPLICATION:

PRIOR APPLICATION

TIME DATE:

CLASSIFICATION:

CLASSIFICATION:

CLASSIFICATION: US-09-407-562-6

```
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSIEL-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1001 New York Avenue, Suite 1000
CITY: Washington STATE: FOODS
CONVENTE EACH OF COMPALIABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: O7-JUN-1995
CLASSIFICATION DATA: APPLICATION DATA:
APPLICATION NUMBER: US 08/215,033
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19-MAR-1994
PRIOR APPLICATION NUMBER: 19-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.2; DB 1; Length 16; Pred. No. 15; 0; Mismatches 3; Indels
                                                                                                                   24884-109348-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 23, Application US/08487033; Patent No. 5739027
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFRERNCK/DOCKET NUMBER: 2488:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
TELEFAX: 202-962-8300
                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: NO GENOMIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.2%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 CGTGTACAGGGAGTCC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORIGINAL SOURCE:

) ORGANISM: Homo sapiens

US-08-474-177-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-487-033-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 43.6%; Score 12.2; DB 1; Length 18; 1 Similarity 82.4%; Pred. No. 10; 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SCALLICK, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPRESSE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: L201 New York Avenue, Suite 1000
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOCTWARE: PATENTIN Release #1.0, Version #1.30
SOCTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/474,177
FILING DATE: 17-WAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 10-JWN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 10-JWN-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 10-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUTCATION INFORMATION:
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
DESCRIPTION: other nucleic acid
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 TGTACAGGGAGTCCAGG 28
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Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-474-177-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
US-09-407-562-6
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40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Storen
APPLICANT: Analy, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: WTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: WEALINGTON

STATE: DC

COUNTRY: USA

ZIF: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/508,735

FILING DATE:
CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/508,735

FILING DATE:
CLASSIFICATION DATA:

APPLICATION NUMBER: US to be assigned

FILING DATE: 07-4MN-1995

FILING DATE: 17-MR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.

REGISTRATION NUMBER: 24884-109348

TELERCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBERHONE: 202-962-4448
REFERENCE/DOCKET NUMBER: 24884-109348
                     TELECOMMUNICATION INFORMATION:
TELEPRAN: 202-962-4810
TELEPRAN: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
                                                                                                                                                                          TYPE: nucleic acid
STANDENNES: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 CGTGTACAGGGAGTCC 25
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SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-480-810-23
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MOLECULE TYPE: DN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-508-735-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 40.0%; Score 11.2; DB 1; Length 16; 1. Similarity 81.2%; Pred. No. 15; 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE S: ADDRESS:
ADDRESSES: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLAD FOCOMPATIBLE
COMPUTER: PROPY disk
COMPUTER: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
RILNG DATE: 07-JUN-1994
FILING DATE: 01-JUN-1994
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA: 14-APR-1994
PRIOR APPLICATION DATA: 14-APR-1994
PRIOR APPLICATION DATA: 14-APR-1994
PRIOR APPLICATION DATA: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: INHER, 78: 28,957
REGISTRATION NUMBER: 28,957
NAME: Ihnen, Jeffrey L.
REGISTRATION UNDERS: 28,957
REFERENCE/DOCKET NUMBER: 24844-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
TELEPAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TYPE: mucleic acid
TYPE: MUCLEICHEITCAL: NOA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/08480810 Patent No. 5801236 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 CGTGTACAGGGAGTCC 25
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                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 13; Conserva
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STRANDEDNESS: single
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Patent No. 5969815

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCANON-Albright, Lisa A.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alaxander.
ITILE OF INVENTION: GENMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: GENERAL OF DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESCENDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Weshington
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                             Query Match 40.0%; Score 11.2; DB 1; Length 16; Best Local Similarity 81.2%; Pred. No. 15; Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
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CLASSIFICATION:
PRICATION:
PRICATION:
PRICATION NUMBER: US 08/474,083
FILING DATE: 07-UM-1995
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-UM-1995
APPLICATION NUMBER: PCT/USS5/03537
FILING DATE: 07-UM-1994
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UWN-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-WAR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-WAR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: 18-WAR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: 18-WAR-1994
ATTORNEY/AGENT INPORMATION:
APPLICATION NUMBER: 28,957
RECISTRATION NUMBER: 28,957
RECISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
FELENCOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                        1 cererceaceasece 16
                                                                                                                                                                                                                                                                                                                                                     10 CGTGTACAGGGAGTCC 25
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-508-735-23
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US-08-848-251-23
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PODECOLE TYPE: DNA (genomic)

MITTARESTOLL: NO

MITTARESTOLL: NO

OGNAMINESTOLL: NO

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,252
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24884-109348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-UN-1995
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 01-UN-1994
FILING DATE: 01-UN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
FILING DATE: 19-MAR-1994
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                            10 CGTGTACAGGGAGTCC 25
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
   ; ANTI-SENSE: YES; ORIGINAL SOURCE: ; ORGANISM: HorUS-09-120-130-23
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US-09-120-130-23
Sequence 23, Application US/09120130
Fatent No. 6037462
Fatent No. 6037462
Fatent No. 8037462
FATILE OF INVENTION:
APPLICANT: Kamb, Alexander
FITILE OF INVENTION:
MUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTY: USA
ZIP.
                                                                                                                                                                                                                                 DB 1; Length 16;
                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: USAS

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPEY disk
COMPUTER: IBM PC compatible
SOCTAME: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130

FILING DATE:
PRIOR APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-UNN-1994

PRIOR APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION NUMBER: US 08/215,086

FILING DATE: 14-APR-1994

PRIOR APPLICATION NUMBER: US 08/217,369

FILING DATE: 14-APR-1994

PRIOR APPLICATION NUMBER: US 08/214,582

FILING DATE: 14-APR-1994

PRIOR APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

PRIOR APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

PRIOR APPLICATION NUMBER: 28/957

REGISTRATION NUMBER: 28/957

REFERENCE/DOCKET NUMBER: 28/957

REPERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                                              Query Match

40.0%; Score 11.2; D

Best Local Similarity 81.2%; Pred. No. 15;

Matches 13; Conservative 0; Mismatches
; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO; ANTI-SENSE: YES; ORIGINAL SOURCE: ORIGINAL SOURCE: CRGNISM: Homo sapiens US-08-486-047-23
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Gaps
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0
Query Match 40.0%; Score 11.2; DB 1; Length 16; Best Local Similarity 81.2%; Pred. No. 15; Matches 13; Conservative 0; Mismatches 3; Indels
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) Sequence 23, Application US/08986515
) Patent No. 6096578
) Patent No. 6096578
) APPLICANT: Kamb, Alexander
) APPLICANT: Kamb, Alexander
) TITLE OF INVENTION: MISI GENE
) NUMBER OF SEQUENCES: 36
) CONRESPONDENCE ADDRESS:
) ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: DC
) CITY: Mashington
) STATE: DC
) STATE: DC

COUNTRY: USA
                                                                                                                                       DB 1; Length 16;
                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:

ZTP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Date Compatible
CURRENT APPLICATION DATE:
FILING DATE: CLASSIPPATION
PRIOR APPLICATION NUMBER: US 08/480,810
FILING DATE: 01-UN-1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 10-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 10-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 10-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 10-MAR-1994
PRIOR APPLICATION NUMBER: 24884-109348
FILING DATE: 10-MAR-1994
PRIOR APPLICATION NUMBER: 24884-109348
FILING DATE: 10-MAR-1994
PRIOR APPLICATION NUMBER: 24884-109348
FILING DATE: 10-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGESTRATION FOR EXC ID NO: 23:
ENGURENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TELEPHONE: 202-962-830
INFORMATION FOR EXC ID NO: 23:
STRANDEDNIESS: stinds
STRANDEDNIESS: stinds
STRANDEDNIESS: stinds
STRANDEDNIESS: stinds
STRANDEDNIESS: Stinds
STRANDEDNIESS: Stinds
MOLECULE TYPE: DNA (genomic)
HYPDTHETICAL: NO
AMTI-SENSE: YES
                                                                                                                                 Query Match
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                            10 CGTGTACAGGGAGTCC 25
                                                                                                                                                                                                                                                                                          1 cererceaseasece 16
; ANTI-SENSE: YES
; CARGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-115-252-23
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US-00-366-1-23

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ORGANISM: Homo sapiens
US-09-201-139-23
; ORGANISM: Homo sapiens
US-09-120-129-23
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Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ठे
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US-09-120-129-13

US-09-120-129-13

Sequence 23, Application US/09120129

Patent No. 6180776

GENERAL INFORMATION:

HITLE OF INVENTION:

TITLE OF INVENTION:

COUNTRY:

COUNTRY:

COUNTRY:

CONTRESPONDENCE NOBESS:

ADDRESSEE: Venable, Basejer, Howard & Civiletti, LLP

STERET: 1201 New York Avenue, Suite 1000

COUNTRY:

CONTRY:

                                                                                Query Match
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-962-4810
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs TYPE: mucleic acid STRANDENESS: single TOPOLOGY: linear MOLECHIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: YES ORIGINAL SOURCE:
                                                                                                                                                                                                              10 CGTGTACAGGGAGTCC 25
                                                                                                                                                                                                                                                                     1 cererchedahecec 16
      Homo sapiens
; ORGANISM:
US-09-120-128-23
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Query Match milarity 40.04; Score 11.2; DB 1; Length 16; Beat Local Similarity 40.04; Score 11.2; DB 1; Length 16; Beat Local Similarity 40.24; Pred: No. 15; Beat Local Similarity 40.24; Pred: No. 15; Beat Local Similarity 40.24; N. 15; Beat Local Similarity 40.24; N. 15; Beat Local Similarity 40.25; Db 1 conformation UN/09201139

**BESTUT 71

**BERTAL INFORMATION: Stoce Steven APPLICATION: Stoce Steven APPLICATION APPLICATION: Stoce Steven APPLICATION APPLICATION
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Score 10.8; DB 1; Length 15; Pred. No. 17;
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Fatent No. 5869253
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE O
REBULT 23
US-08-182-68A-121
Sequence 121, Application US/08182968A
Patent No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: MHHBITING HERAITIS C
TITLE OF INVENTION: NHHBITING HERAITIS C
TITLE OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: Suite 4700
CUNTRY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35." Diskette, 1.44 Mb
MEDIUM TYPE: 35." Diskette, 1.44 Mb
MEDIUM TYPE: 35." Diskette, 1.44 Mb
MEDIUM TYPE: 31." JOHNURY-1994
FILING DATE: 13-JANUARY-1994
FILING DATE: 13-JANUARY-1994
FILING DATE: 13-JANUARY-1994
FRICK RPPLICATION NUMBER: 37.37
FILING DATE: 14-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32.32
TELEFRA: (213) 955-0440
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 15.5.1
LENGTH: 15.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
38.6%; Score 10.8; D
Best Local Similarity 71.4%; Pred. No. 17;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGGCCCTACGTGTA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ĠĠĠĊĊĊUCĊĠŪĠCĂ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
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US-08-774-306A-121
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     WESULT 22
UG-09-120-131-23
UG-09-120-131-23
UG-09-120-131-23
FAGGETOR 23 Application US/09120131
FAGGETOR 23 Application US/09120131
FAGGETOR 23 Application US/09120131
FAGGETOR 20 ENTERNION: WITS GENE
NUMBER OF ENCINEES: 36
CORRESSEE: JOOD WAYER Avenue, Suite 1000
STREE: 1201 New York Avenue, Suite 1000
STREE: 1201 New York Avenue, Suite 1000
STREE: DCCONTRY: UGA
ZIP: 2005
CONTRY: UGA
ZIP: PROBABLE FORM:
WEILING TYPE: RIOPPY disk
CONTUTER: REALIN Release #1.0, Version #1.30
FRING APPLICATION NUMBER: US/09/120,131
FILING DATE: 17-44R-1995
FILING DATE: 17-44R-1995
FILING DATE: 17-44R-1994
FRICK APPLICATION NUMBER: US 08/215,087
FILING DATE: 11-44R-1994
FRICK APPLICATION NUMBER: US 08/214,582
FILING DATE: 11-44R-1994
FRICKANDER: US 08/214,582
FILING DATE: 11-44R-1994
FRICKANDER: US 08/214,582
FILING DATE: 11-44R-1994
FRICKANDER: US 08/214,093
FRIERAR: 202-962-448
FRICKANDER: US 08/214,093
FRIERAR: 202-962-448
FRIERAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 CGTGTACAGGGAGTCC 25
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Gaps

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Indels

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Mon Apr 19 15:55:12 2004
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US-09-081-646-637/c

US-09-081-646-637/c

Sequence 637, Application US/09081646

Patent No. 6333152

GENERAL INFORMATION:

APPLICANT: Kinzler, Kenneth

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

APPLICANT: Chang, Lin

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Cancer Cells

TITLE NETRING DATE: 1998-05-20

EARLIER APPLICATION NUMBER: 60/047,352

EARLIER FILING DATE: 1997-05-21

NUMBER OF SEQ ID NOS 871

SOFTWARE: FastSEQ for Windows Version 3.0

TEMBER OF SEQ ID NOS 871

SEQ ID NO 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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US-09-180-437-185
Sequence 185. Application US/09180437
Patent No. 6251873
Patent No. 6251873
GENERAL INFORMATION:
APPLICANT: FUKUSAKO, Shioji
APPLICANT: MCSURAWA, Yoshifumi
APPLICANT: MCSURAWA, Takeshi
TITLE OF INVENTION: Antisense Compounds to CD14
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT FILING DATE: 1998-11-06
EARLIER PLING DATE: 1998-03-09
EARLIER PLING DATE: 1998-03-09
EARLIER PLING DATE: 1998-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.6%; Score 10.8; Di
Best Local Similarity 71.4%; Pred. No. 17;
Matches 10; Conservative 2; Mismatches
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85.7%; Pred. No. 17;
tive 0; Mismatches
                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERINCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INVORMATION:
TELEPHONE: (213) 955-0440
TELEPAX: (213) 955-0440
ITELERX: 67-3510
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 ACAGGGAGTCCAGG 28
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-064-156A-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-637
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Sequence 121, Application US/09064156A
Sequence 121, Application US/09064156A
Sequence 121, Application US/09064156A
GENERAL INFORMATION: Remeth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: URBERTICATION UNMER OF SEQUENCES: 498
CORRESPONDENCES: 498
CORRESPONDENCES: 498
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: Suite 470
CUTY: Los Angeles
STATE: California
COUNTY: Los Angeles
STATE: California
COUNTY: 1.3.A.
STATE: California
COUNTY: 1.5.A.
COUNTY: 1.5.A.
STATE: CALIFORNIA
MEDIUM TYPE: 3.5." Diskette, 1.44 Mb
MEDIUM TYPE: 3.5." Diskette, 1.44 Mb
MEDIUM TYPE: 81.5." Diskette, 1.44 Mb
MEDIUM TYPE: 81.5." Diskette, 1.44 Mb
MEDIUM TYPE: 40.00 S.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/74,306
FILING DATE: APALIA, 1998
FILING DATE: December 26, 1996
FILING DATE: DATE: APALIA, 1991
FILING DATE: MAY 14, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.4%; Pred. No. 17;
Matches 10; Conservative 2; Mismatches
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: Storage
COMPUTER: Storage
COMPUTER: BW Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: MANUAL:
APPLICATION NUMBER: 07/082,968
FILING DATE: MAY 14, 1992
APPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: G-3510
INPORMATION FOR SEQ ID NO: 121:
SEQUENCE GHARACTERISTICS:
LENGTH: 15
FUNDER GHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGCCCCCGUGCA 14
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-121
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RESULT 29
US-08-319-492B-24
'S Sequence 24, Application US/08319492B
'Patent No. 5616488
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                                                                                                                     TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:other nucleic
COTHER INFORMATION: acid
US-09-180-437-185
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                 Query Match 37.1%; Score 10.4; DB 1; Length 15; Best Local Similarity 91.7%; Pred. No. 23; Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-182-968A-297

Sequence 297, Application US/08182968A

Patent No. 5610054

GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: URUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENTS ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE AUDACESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: LOS Angeles
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-206 FORM:
MEDIUM TYPE: Storage
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,968A
FILING DATE: 13-0ANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGESTRATION NUMBER: 205/277
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 67-3510
INFORMATION FOR SEQ ID NO: 297:
SEQUENCE CHARACTERISTICS:
EARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 185
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                     17 AGGGAGTCCAGG 28
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STRANDEDNESS: sing
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Diager. Kenneth G.
APPLICANT: Diager. Kenneth G.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
ITTLE OF INVENTION: REOXYME TREATMENT OF DISEASES
TITLE OF INVENTION: OF CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF LL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 90071
ZONDUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: SONDELS
COMPUTER: BECOMBELIO
COMPUTER: BECOMBER: BECOMBELIO
COURRENT APPLICATION DATA:
APPLICATION NUMBER: BECOMBELIO
FILING DATE: COCCODER: T, 1994
FILING DATE: DECEMBER: O1/899, 849
FILING DATE: DECEMBER: 7, 1992
APPLICATION NUMBER: 30/899, 849
FILING DATE: DECEMBER: 7, 1992
APPLICATION NUMBER: 32,327
REFERENCE/POCKET NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kenneth G.
METHOD AND REAGENT FOR
INHIBITING HEPATITIS C
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Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper:
APPLICANT: Draper:
TITLE OP INVENTION: METHOD AND REAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0
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US-08-319-492B-24
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US-08-774-306A-297
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Gaps

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19 GGAGTCCAGG 28

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Sequence 38, Application US/09698505A
Setent No. 6479242
GENERAL INFORMATION:
APPLICANT: GAO, Bacchuan
TITLE OF INVENTION: A No. 6479242el Method for Genotyping of Single Nucleotide Polyn
FILE REFERENCE: 27433/04001
CURRENT APPLICATION NUMBER: US/09/698,505A
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
LENGTH: 14
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Pred, No. 29;
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US-08-182-968-115
US-08-182-968-115
Sequence 115, Application US/08182968A
PACENT No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: URUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9.8; DB
Pred. No. 29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,156A
FILING DATE: APPLI 21, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: MAY 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: (213) 489-1600
TELERAX: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
SEQUENCE CHARACTERISTICS:
LENGTH: 15
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 84..
Local 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GGAGTCCAGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGAGUCCAGG 12
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CORGANISM: A Homozygote
US-09-698-505A-38
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US-09-698-505A-38/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 297, Application US/09064156A
Sequence 297, Application US/09064156A
Sequence 297, Application US/09064156A
TITLE OF INVENTION: WHITHENTH HERALITIS C
TITLE OF INVENTION: WHITHENTH HERALITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 498
COMBERGENOMERS: 498
COMBERGENOMERS: ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 631 West Fifth Street
STREET: 631 West Fifth Street
STREET: California
COUNTRY: US.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDLIM TYPE: 3.5" Diskette, 1.44 Mb
MEDLIM TYPE: BLOADELE
                    FITTE OF INVENTION: VIRUS REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GGAGTCCAGG 28
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US-08-774-306A-297
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US-09-064-156A-115
Sequence 115, Application US/09064156A
Patent No. 6132966
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: URUS REPLICATION
NUMBER OF SEQUENCES: 498
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 233/227
TELECOMMINICATION INFORMATION:
TELEPHONE: (213) 489-160
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 115:
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (213) 489-1600
(213) 955-0440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ścececuacionana 14
                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                       ;
US-08-774-306A-115
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Sequence 115, Application US/08774306A

Patent No. 586325A

Patent No. 586325A

Patent No. 586325A

TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HERATITIS C TITLE OF INVENTION: INHIBITING HERATITIS C TITLE OF INVENTION: VIRUS REPLICATION NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS: Apon & Lyon & Lyon STREET: 63 West fifth Street STREET: Suite 4700

CITY: Los Angeles STREET: Suite 4700

CONTRY: US.A.

ZIP: 90071-2066

COMPUTER RALDABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: STREET

COMPUTER: EMDADLE SECTAGE

COMPUTER: DOCOMPER: DOCOMPER: US/08/774,306A

PRICATION NUMBER: US/08/774,306A

PRICATION NUMBER: 08/182,968
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35.0%; Score 9.8; DB
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: 18M Compactible
COMPUTER: 18M Compactible
OPERATING SYSTEM: 18M P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,968A
FILING DATE: 13.4AMUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14.4MY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
RESTERENCE/DOCKET NUMBER: 205/277
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE:
SEQUENCE STATEMENTICS:
TENERY: 67-3510
    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GGCCCTACGTGTA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: single
                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
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TOPOLOGY: linear

US-08-182-968A-115
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PAPLICANT: REENNAN, THOMAS M.

TITLE OF INVENTION: APPARATUS FOR DETERMINING DNA SEQUENCES
BY MASS SPECTROMETRY

CURRENT APPLICATION DATA:

PRILIG DATE: 20-UUN-1989

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 15;
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US-09-203-231B-67
Sequence 67, Application US/09203231B
Patent No. 635523
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan M
APPLICANT: Hu, Xinghua
ITLE OF INVENTION: Methods and Devices for Measuring
ITLE OF INVENTION: Methods and Devices for Measuring
ITLE OF INVENTION: Differential Gene Expression
FILE REFERENCE: 7934-052
CURRENT APPLICATION NUMBER: US/09/203,231B
CURRENT FILING DATE: 1998-12-02
PRIOR FILING DATE: 1997-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
35.0%; Score 9.8; DB
Best Local Similarity 84.6%; Pred. No. 33;
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 9.4; Di
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 67
LENGTH: 12
              CLASSIFCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
NAME: Lunn, Paul, G.
REGISTRATION NUMBER: 32,743
REGISTRATION NUMBER: 32,743
REFERENCE, POCKET NUMBER: JB0255
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-822-7039
TELERAX: 201-822-7039
TELEX: 219165
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 CAGGGAGTCCAGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.6
Best Local Similarity 90.5
Matches 10; Conservative
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COTHER INFORMATION: Primer US-09-203-231B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 cadddaacccadg 3
  19930326
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PCT-US93-02612-2
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Sequence 2, Application PC/TUS9302612

Sequence 2, Application PC/TUS9302612

Sequence 2, Application PC/TUS9302612

Sequence 2, Application PC/TUS9302612

SENERALINEORATION:
Mannatino, Mithony
TITLE OF INVENTION:
Monomeric Platelet-Derived Growth Factor and Prevention of NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSED: Schering-Plough Corporation
STREET: One Giralda Farms
CITY: Madison
STREET: New Jersey
COUNTR: USA

CONDYTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
CORPUTER: Microsoft Word 4.00B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02612
                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:other nucleic
US-09-180-437-134
                                                                                                                                                               ..
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                                                                                                              Score 9.8; DB 1; Length 15; Pred. No. 33; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 1134, Application US/09180437

Patent No. 6251873

GENERAL INVORMATION:
APPLICANT: FUKUSAKO, Shioji
APPLICANT: MORIGAWA, Yoshifumi
APPLICANT: MUSTYAMA, Takeshi
TITLE OF INVENTION: Antisense Compounds to CD14
FILE REFERENCE: 1110-209P
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT FILING DATE: 1998-03-09
EARLIER FPLING DATE: 1998-03-09
EARLIER FILING DATE: 1999-03-09
SARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 134
LENGTH: 15
                                                                                                              Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGCCCTACGTGT 14
                                                                                                                                                                                                         3 GGCCCTACGTGTA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 GCGCCCTGCGTGT 1
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-064-156A-115
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US-09-180-437-134/c
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5174962-40
5174962-40
5174962-40
7 PAPLICANT: BRENNAN, THOMAS M.
7 TITLE OF INVENTION: APPARATUS FOR DETERMINING DNA SEQUENCES
7 NUMBER OF SECTROMETRY
7 NUMBER OF SEQUENCES: 2
7 CURRENT APPLICATION DATA:
7 FILING DATE: 20-JUN-1989
7 FILING DATE: 20-JUN-1989
7 PRIOR APPLICATION DATA:
7 PRIOR APPLICATION DATA:
7 PRIOR APPLICATION DATA:
7 PRIOR APPLICATION NUMBER: 209,247
7 PRILING DATE: 20-JUN-1989
7 PRILING DATE: 20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 9.4; DB 1; Length 12;
Pred. No. 27;
0; Mismatches 1; Indels
                                                                                                                                            33.6%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 27; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08623891
Fatent No. 579578
CEMBRAL INFORMATION:
TITLE OF INVENTION: INFIBITING HERPES SIMPLEX
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READMBLE FORM:
COMPUTER READMBLE FORM:
MEDINA TYPE: 3." Diskette, 1.44 Mb storage
COMPUTER: 1EM Compatible
OPERATING SYSTEM: 1EM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/238,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:

PAPLICATION NUMBER: US/07/987,133
FILING DATE:
APPLICATION NUMBER: 07/882,921
## APPLICATION NUMBER: 209,247
### FILING DATE: 20-UUN-1988
### SEQ ID NO:2:
### LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.6
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                         Conservative
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                                                                                                                                                                   Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 12
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:2
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PILLING DATE: May 14, 1922

ATRIANG NAMES: 07/948,359

ATRIANG NAMES: 07/948,359

ATRIANG NAMES: 07/948,359

ATRIANG NAME NAMES: 07/948,359

ATRIANG NAMES: 04/94,061

ATRIANG NAMES: NAMES: 04/94,061

ATRIANG NAMES: 04/94,061

ATRIANG NAMES: NAMES: 04/94,061

ATRIANG NAME: NAMES: 04/94,061

ATRIANG NAMES: 04/94,061
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Patent No. 585461

GENERAL INFORMATION:
APPLICANT: Colote, Soudhir
APPLICANT: Pirotzky, Eduardo
TITLE OF INVENTION: Oligonucleotides to Inhibit the
TITLE OF INVENTION: Expression of Isopremyl Protein Transferases
NUMBER OF SQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Lucas & Just
STRETT: 205 E. 42nd Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM 466 Compatible
COMPUTER: IBM 466 Compatible
COMPUTER: IBM 466 Compatible
COMPUTER: 1.44 MB storage
COMPUTER: 1.44 MB 10025 5.0
CURRESTEICATION NUMBER: USA 1.4
APPLICATION NUMBER: USA 1.4
APPLICATION NUMBER: GB 9413035.8
FILING DATE: 23-JUNE-1994
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1.2 base pairs
TYPE: HIGH TAPE: DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
32.1%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches
; Sequence 6, Application US/08494301A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleotide STRANDEDNESS: single TOPOLICGY: linear ANTI-SENSE: Yes US-08-494-301A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GTACAGGGA 21
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0
                                                                                            Score 9.2; DB 1; Length 14; Pred. No. 42; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                               US-09-614-262-20/C
US-09-614-262-20/C

Sequence 20, Application US/09634262

Sequence 20, Application US/09634262

Sequence 20, Application US/09634262

GENERAL INFORMATION:

TITLE OF INVENTION: METHOD AND REAGENT FOR

TITLE OF INVENTION: INHIBITING HERPES SIMPLEX

TITLE OF INVENTION: VIRUS REPLICATION

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/634,262
FILING DATE:
CLASSIFICATION TO DATA:
APPLICATION NUMBER: US/07/987,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9.2; DB
Pred. No. 42;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PHILOR DATE:
APPLICATION NUMBER: 07/882,921
FILING DATE: MAY 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELESAX: (213) 955-040
TELEX: 67-3510
INFORMATION FOR SEG ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                            Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                                                                        10 CGTGTACAGGGAGT 23
                                                                                                                                                                                                                            14 CGTGATCAGGGCGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-340-861-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
US-09-634-262-20
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0; Indels Length 12;

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Score 8.8; DB 1; Length 12; Pred. No. 40;
31.4%;
83.3%;
                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                       ; OTHER INFORMATION: Primer US-09-203-231B-67
                                                                                                                                           Query Match
Best Local Similarity
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Gaps

.; 0

3; Indels

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RESULT 44 US-08-494-301A-6/c

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patent No. 6632057

GENERAL INFORMATION:
APPLICANT: BHAW, LINN C.
APPLICANT: SHAW, LINN C.
APPLICANT: GRAM, LINN C.
APPLICANTON: THE TREATMENT OF RETINAL DISEASES
TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100
CURRENT APPLICATION NUMBER: 09/063,667
PRIOR PELICATION NUMBER: 09/063,667
PRIOR PELICATION NUMBER: 60/046,147
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PALENTING DATE: 1997-04-21
SEQ ID NO 30
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.4%; Score 8.8; DB 1; Length 13; 66.7%; Pred. No. 47; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-19-942-7/c

1 Sequence 7, Application US/08192942

1 Sequence 7, Application US/08192942

1 Patent No. 5989906

1 Patent No. 5989906

1 TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INSTRUCT ON TITLE OF INVENTION: INSTRUCT ON TITLE OF INVENTION: INSTRUCT ON TITLE OF INVENTION: I GENE TITLE OF INVENTION & LYON & LYON & STREET: California COUNTRY: USA APPLICATION DATA: NORDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: READABLE ON THE STORY ON TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: WORDPATIBLE OPERATION SYPEM: IBM P.C. DOS (Version 5.1)

CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/07/882,885

FILING DATE: TITLING DATE: TITLING DATE: ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 32,327

RECISTRATION NUMBER: 32,327

REPERENCE/DOCKET NUMBER: 197/173

TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ). NAME/KEY: misc feature

; LOCATION: ()..()

; COTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

MS-09-874-601-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGGGCCCTACGT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 cadecucuaceu 12
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                                                                                                                                                                         RESULT 46

105-09-281-11/C

105-09-281-11/C

Sequence 211, Application US/09281418

Sequence 211, Application US/09281418

Sequence 211, Application US/09281418

JETER NO. 6287769

JETER NOTAMIT: Inoue, Tatakazu

JITLE OF INVENTION: Amplifying DNA Fragment, Apparatus for Amplifying DNA F

JITLE OF INVENTION: Amplifying DNA Fragment, Apparatus for Amplifying DNA F

JITLE OF INVENTION: Amplifying DNA Fragment, Method of Assaying Contaminant

FILE REPERENCE: 9982-7

CURRENT APPLICATION NUMBER: UP/1998/87651

SEALIER APPLICATION NUMBER: UP/1999/69694

SEALIER APPLICATION NUMBER: UP/1999/69694

SEALIER PILING DATE: 1999-03-16

NUMBER OF SEQ ID NOS: 216

SEQ ID NO 211

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Patent No. 6063573
GENERAL INFORMATION:
APPLICANT: Kayyem, Cayling Probe Technology Using Blectron Transfer TITLE OF INVENTION: Cycling Probe Technology Using Blectron Transfer TITLE OF INVENTION: Detection
TITLE OF INVENTION: Detection
FILE REPRESENCE: A65697/RFF/RMS/RMK
CURRENT APPLICANON NUMBER: US/09/014,304
CURRENT FILING DATE: 1998-01-27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence FEATURE: ORGANISM: ORGANISM: Artificial Sequence: synthetic US-09-014-304-3
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31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8.8; DB 1; Length 12; Pred. No. 40; 0; Mismatches 2; Indels
2; Indels
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
CHER INFORMATION: Primer
US-09-281-418-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 ACGTGTACAGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACGTGTCCATGG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 CCCTACGTGTAC 16
10; Conservative
                                                     13 GTACAGGGAGTC 24
                                                                                          12 GTACAGGTAGGC 1
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US-09-874-601-30
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RESULT 47 US-09-014-304-3

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Sequence 30, Application US/09874601

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Matches

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30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic US-09-326-186B-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GTACAGGGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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US-08-777-266A-85/c
US-08-777-266A-85/c
IS-08-777-266A-85/c
Sequence 85, Application US/08777266A
Patent No. 6077833
GENERAL INFORMATION:
PAPLICANT: Clarence Frank Bennett
APPLICANT: Timothy A. Vickers
ITILE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
ITILE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive Bast, Suite 201
CITY: Cherry Hill
COUNTRY: USA
ZID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.0%; Score 8.4; DB 1; Length 10; ilarity 90.0%; Pred. No. 35; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 08002
COMPUTER READALE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/777,266A
FILING DATE: DOcember 31, 1996
PLION APPLICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.0%; Score 8.4; DB Best Local Similarity 90.0%; Pred. No. 35; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 1SPH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-2400
TELEPAX: (609) 779-2400
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHRACTERISTICS:
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 'SEQUENCE CHARACTERISTICS:
LENGTH: 100
                        (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-192-942-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-777-266A-85
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Sequence 14, Application US/09769482

| Sequence 14, Application US/09769482
| Patent No. 6566130
| General Information:
| APPLICANT: SAIVASTAVA, SHIV
| APPLICANT: MOLL, JUDD W.
| APPLICANT: WU, LINDA L.
| APPLICANT: XV, LINDA L.
| APPLICANT: SEGAMA, TAKEHIKO
| TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
| TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
| TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
| FILE REFERENCE: 04995.0657-00000
| CURRENT APPLICATION WHMER: US/09/769, 482
| CURRENT FILING DATE: 2000-01-26
| PRIOR APPLICATION NUMBER: 60/179, 772
| PRIOR APPLICATION NUMBER: 60/179, 745
| PRIOR APPLICATION NUMBER: 60/179, 045
| PRIOR APPLICATION NUMBER: 60/179, 045
| PRIOR APPLICATION NUMBER: 60/179, 045
| PRIOR PRIOR DATE: 2000-01-31
| SEQ ID NO 14
| LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: oligonucleotide
US-09-769-482-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 8.4; DB 1; Length 10, Pred. No. 35; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GTACAGGGAG 22
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US-08-777-266A-86/c
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Query Match 30.0%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 43; Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: 00466.78503
CURRENT FILING DATE: 1999-02-12
CURRENT FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-09-28
PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 346
NUMBER OF SEQ ID NOS: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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US-08-623-891-39

Sequence 39, Application US/08623891

Sequence 39, Application US/08623891

Sequence 39, Application US/08623891

Sequence 39, Application US/08623891

TITLE OF INVENTION: MITHOR REAGENT FOR TITLE OF INVENTION: INHIBITING HERPES SIMPLEX ITILE OF INVENTION: VIRUS REPLICATION

TITLE OF INVENTION

TITLE OF INVENTION

TITLE OF INVENTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.0 Diskette, 1.44 Mb storage
(MODIUM TYPE: 13M Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WoordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8.4; DB
Pred. No. 43;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-249-155A-45/c
; Sequence 45; Application US/09249155A
; Patent No. 65381/3
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.0%;
                                                                                                           ; OTHER INFORMATION: Synthetic US-09-326-186B-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTACAGGGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GTACAGGGAG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 GTACGGGGAG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-249-155A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 45
LENGIH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
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APPLICANT: Clarence Frank Bennett
APPLICANT: Clarence Frank Bennett
TITLE OF INVENTION: Oligonucleotide Compositions and
TITLE OF INVENTION: Oligonucleotide Composition of the Expression of B7 Proteins;
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins;
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSBE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive Bast, Suite 201
CITY: Cherry Hill
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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US-09-326-186B-86/c

Sequence 86, Application US/09326186B

Patent No. 6319906

GENERAL INFORMATION:
APPLICANT: Bennett, Clarence Frank
APPLICANT: Wickers, Timothy A.
TITLE OF INVENTION: Oligonuclectide Compositions and Methods for the
TITLE OF INVENTION: Modulation of the Expression of B7 Protein
FILE REPRENCE: ISPH-0376
CURRENT APPLICATION NUMBER: US/09/326,186B
CURRENT APPLICATION NUMBER: US/09/326,186B
CURRENT APPLICATION NUMBER: 08/777,266
PRIOR PILING DATE: 1996-12-31
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 86
LENGTH: LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM P8/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: MORDERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,266A
FILING DATE: December 31, 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                    Sequence 86, Application US/08777266A
Parent No. 6077833
GENERAL INFORMATION:
APPLICANT: Clarence Frank Bennett
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0
Best Local Similarity 90.0
Matches 9; Conservative
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STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 GTACAGGGAG 22
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ANTI-SENSE: Yes

US-08-777-266A-86
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Sequence 28, Application US/08494301A

Datent NO. 5856461

GENERAL INFORMATION:
APPLICANT: COlote, Soudhir
APPLICANT: Pirotzky, Eduardo
TITLE OF INVENTION: Oligonucleotides to Inhibit the
TITLE OF INVENTION: Expression of Isoprenyl Protein Transferases
NUMBER OF SEQUENCES:
ADDRESSE: Lucas & Just
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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Pred. No. 51;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: 1EM 486 COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,301A
FILING DATE: 23-UTNE-1995
CLASSIFICATION NUMBER: GB 9413035.8
FILING DATE: 29-UTNE-1994
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base paire
              FILING DATE:
APPLICATION NUMBER: US/07/987,133
FILING DATE:
APPLICATION NUMBER: 07/882,921
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTATION NUMBER: 32,327
REGISTATION NUMBER: 32,327
APPLICATION NUMBER: US/08/238,200
                                                                                                                                                                                                                         200/209
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It Lucas & Just
205 E. 42nd Street
                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%;
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Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ccccaccucu 10
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US-08-623-891-39
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CITY: New York
STATE: New York
COUNTRY: USA
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10017
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30.0%; Score 8.4; DB 1; Length 12;

Query Match

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Sequence 107, Application US/09281418
Patent No. 6287769
GENERAL INFORMATION:
APPLICANT: Income, Takakazu
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA
TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing M
TITLE OF INVENTION: niems and Method of Assaying Contaminant
FILE REPERENCE: 9982-7
CURRENT APPLICATION NUMBER: US/09/281,418
                                                                                                                                                                                                                                        Sequence 87, Application US/08777266A
Patent No. 6077833
GENERAL INFORMATION:
FOR INCOMPAINT:
CLIATE OF INVENTION:
O'IL GOVERS
TITLE OF INVENTION:
O'IL GOVERS
CORRESPONDENCE:
CORRESPONDENCE ADDRESS:
ADDRESSE:
Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY:
CHETY CHETY H111
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                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 51;
Pred. No. 51;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,266A
FILING DATE: December 31, 1996
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER:
PILING DATE:
PILING DATE:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: JANE MASSEY LICATE
REGISTRATION NUMBER: 32,257
REFERENCE/POCKET NUMBER: 1SPH-0201
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-2400
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-2400
TELEFAX: (609) 779-2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.0%; Score 8.4; 90.0%; Pred. No. 5
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                          9 ACGTGTACAG 18
                                                                                                                          11 ACGAGTACAG 2
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STRANDEDNESS:
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COUNTRY: U
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APPLICANT: MISSULANT: ALEMENT
APPLICANT: MISSULANT: MISSULANT: MISSULANT: MISSULANT: MISSULANT: MARK
APPLICANT: MASS, STEVEN H.
APPLICANT: WESC, JON E.
APPLICANT: WESC, JON E.
APPLICANT: GUSTAFSSON, CLAES
APPLICANT: PATTEN, PHILLIP A.
TITLE OF INVENTION: OLIGONUCLECTIDE MEDIATED NUCLEIC ACID RECOMBINATION
TITLE OF INVENTION: OLIGONUCLECTIDE MEDIATED NUCLEIC ACID RECOMBINATION
TITLE OF INVENTION: OLIGONUCLECTION MUMBER: US/09/484,850
CURRENT FILING DATE: 2000-01-18
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/141,049
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 25
LENGTH: 12
APPLICANT: Vickers, Timothy A.

TITLE OF INVENTION: Oligonuclectide Compositions and Methods for the TITLE OF INVENTION: Modulation of the Expression of B7 Protein FILE REFERENCE: ISPH-037 8009/326,186B
CURRENT APPLICATION NUMBER: US/09/326,186B
PRIOR APPLICATION NUMBER: 08/777,266
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 87
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.0%; Score 8.4; DB 1; Best Local Similarity 90.0%; Pred. No. 51; Matches 9; Conservative 0; Mismatches 1
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0; Mismatches
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US-09-408-392-25
; Sequence 25, Application US/09408392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/09484850 Patent No. 636861 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CRAMERI, ANDREAS APPLICANT: STEMMER, WILLEM P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.0%;
                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic US-09-326-186B-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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; NAME/KEY: CDS
; LOCATION: (1)..(12)
US-09-484-850-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-484-850-25
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APPLICANT: CRAMERI, ANDREAS
APPLICANT: STEWMER, WILLEM P.C.
APPLICANT: STEWMER, WILLEM P.C.
APPLICANT: MINSHULL, JERENY
APPLICANT: WELCH, MARK
APPLICANT: WELCH, MARK
APPLICANT: WELCH, MARK
APPLICANT: PATTEN, PHILLIP A.
ITHE OF INVENTION: OLIGONUCLECTIOE MEDIATED NUCLEIC ACID RECOMBINATION
FILE REFERENCE: 02-029620US
CURRENT APPLICATION NUMBER: US/09/626,929
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                                                                                                                                                                                                                                                                                                                 DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                               Score 8.4; DB
Pred. No. 51;
0; Mismatches
         CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: JP/1998/87651
EARLIER FILING DATE: 1998-03-18
EARLIER APPLICATION NUMBER: JP/1999/69694
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 216
EENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/408,392
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-00-18
PRIOR PILING DATE: 1999-02-05
PRIOR PILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
LENGTH: 12
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US-09-326-186B-87/c
; Sequence 87, Application US/09326186B
; Patent No. 6319906
; PERERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
                                                                                                                                                                                                                                                                                                                 30.0%;
                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0
                                                                                                                                                                                                                         FEATURE:

COTHER INFORMATION: Primer
US-09-281-418-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GGGAGTCCAG 27
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: CDS
, LOCATION: (1)..(12)
US-09-626-929-25
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Pred. No. 51;
0; Mismatches 1; Indels
                                                                                                     1; Indels
                                                                                      Best Local Similarity 90.0%; Pred. No. 51; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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                                                                                                                                 18 GGGAGTCCAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (1)..(12)
US-09-626-528-25
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US-09-340-861-39
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STEWMER, WILLEW P.C.

STEWMER, WILLEW P.C.

APPLICANT: MINSHULL, JERENY
APPLICANT: WELCH, MARK
APPLICANT: OLIGONUCLECTIDE MEDIATED NUCLEIC ACID RECOMBINATION
TITLE OF INVENTION: OLIGONUCLECTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE OF INVENTION NUMBER: US/09/408,392
CURRENY APPLICATION NUMBER: 60/118,813
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VOET: 2
SEQ ID NO 25
LENGRIH: 12
TYPE: NV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.0%; Score 8.4; DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8.4; DB
Pred. No. 51;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.0
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; CRGANISM: Homo sapiens
; FRATURE:
; NAME/KEY: CDS
; LOCATION: (1).(12)
US-09-408-392-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GGGAGTCCAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 dedegreeag 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
; LOCATION: (1)..(12)
US-09-626-930-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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US-US-DS-LAB

Sequence 25, Application US/09626528

Fatent No. 6436224

GENERAL INFORMATION:

APPLICANT: CRAMERI, ANDREAS

APPLICANT: BASS, STEVEN H.

APPLICANT: BASS, STEVEN H.

APPLICANT: BASS, STEVEN H.

APPLICANT: BASS, JON E.

APPLICANT: WELCH, MARK

APPLICANT: WESS, JON E.

APPLICANT: PATEN, PHILLIP A.

TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION

FILE REPRENCE: 20-20-20-20-6

FRIOR APPLICATION NUMBER: 09/408, 392

PRIOR APPLICATION NUMBER: 60/118, 813

PRIOR FILING DATE: 1999-02-05

FRIOR FRIOR FILING DATE: 1999-02-05

FRIOR FRIOR FILING DATE: 1999-02-05

FRIOR FRIOR FRIOR FRIOR DATE: 1999-03-05

FRIOR FRIOR FRIOR DATE: 1999-03-05

FRIOR FRIOR FRIOR FRIOR DATE: 1999-03-05

FRIOR FRIOR FRIOR FRIOR FRIOR DATE: 1999-03-05

FRIOR FRIOR FRIOR FRIOR DATE: 1999-03-05

FRIOR F
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Sequence 10, Application US/09340861

Sequence 10, Application US/09340861

SEPELIANT: Kenneth G. Draper

TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 115
CORRESSORE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD STOTAGE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Manderfect (Version 5.0)
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STEWMER, MILEM P.C.
APPLICANT: STEWMER, MILEM P.C.
APPLICANT: BASS, STEVEN H.
APPLICANT: BASS, STEVEN H.
APPLICANT: BASS, JON E.
APPLICANT: PATTEN PHILL P.A.
TITLE OF INVENTION: OLIGONUCLECTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE REFERENCE: 02-02620US
CURRENT APPLICATION NUMBER: 05/9626,595
CURRENT FILING DATE: 1999-02-28
FRIOR FILING DATE: 1999-02-28
FRIOR FILING DATE: 1999-02-05
FRIOR PELLON NUMBER: 60/141,049
FRIOR FILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR FILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR PILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR FILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR PILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR PILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR PILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR FILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR FILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/141,049
FRIOR FILING DATE: 1999-02-05
FRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.0%; Score 8.4; DB Best Local Similarity 70.0%; Pred. No. 51; Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09694863; Patent No. 6521453; GENERAL INFORMATION: APPLICANT: CHAMERI, ANDREAS APPLICANT: STEWMER, WILLEM P.C. APPLICANT: MINSHULL, JEREMY APPLICANT: BASS, STEVEN H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/09626595
Patent No. 6479652
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                               TELEPHONE: (213) 489-1600
TELEBERA: (213) 955-0440
TELER: 67-3510
TELER: 77-3510
SEQUENCE CHARACTERISTICS: 399,
ENOURNE CHARACTERISTICS: TENOTH: 12
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: TOPOLICY: linear
TOPOLICY: linear
US-09-634-262-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.0
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 CCCTACGTGT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ccccaccucu 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: CDS
) LOCATION: (1)..(12)
US-09-626-595-25
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US-09-694-863-25
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Pred. No. 51;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/09634262

Sequence 39, Application US/09634262

RELET NO. 6440719

GENERAL INFORMATION:
TITLE OF INVENTION: INHIBITING HERES SIMPLEX
TITLE OF INVENTION: INHIBITING HERES SIMPLEX
TITLE OF INVENTION: URB REPLICATION
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREE: 611 West & Sixth Street
CITY: Los Angeles
STATE: California
COMPURY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIEP 90017

COMPUTER READABLE FORM:
WRDIUM TYPE: 35." Diskette, 1.44 Mb storage COMPUTER: IBM Compatible
CORFUTER: IBM Compatible
ODERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/634,262
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/07/987,133
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/882,921
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY AGENT INFORMATION:
                                         FILING DATE:
CLASSIFICATION:
PRICR APPLICATION:
PRICR APPLICATION
PRICR APPLICATION NUMBER: US/07/987,133
FILING DATE: WAY 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGRAT INFORMATION:
NAME: Warburg, Richard J.
REGISTATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: (213) 955-0440
TELERX: 67-3510
TELEX: 67-3510
TELEX: 67-3510
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TVDR: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCCGACGUGU 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 CCCTACGTGT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-634-262-39
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TELECOMMUNICATION INFORMATION:

15 crccaagracage 3 g

APPLICANT: WELCH, MARK
APPLICANT: WESA, JON E.
APPLICANT: URSS, JON E.
APPLICANT: WESA, JON E.
APPLICANT: BATTEN, DON E.
TITLE OF INVENTION: OLIGONUCLECTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE OF INVENTION: OLIGONUCLECTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE REFERENCE: 0.0.20.20.20.20.20.30.
CURRENT FILING DATE: 2.00.-10.23
PRIOR PLILING DATE: 1999-09-28
PRIOR PLILING DATE: 1999-09-28
PRIOR PLILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 25
LENGTH: 1.2

RESULT 71

US-09-989-789-2098/C

Sequence 2098, Application US/09989789

Patent No. 6588746

GENERAL INFORMATION:

APPLICATION OLAR STRIPLETS BY ZINC FINGERS

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

CURRENT FILENCE 325-0011.20 / \$11-U32

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2098

LENGTH: 9 ; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA
US-09-989-789-2098 Query Match 28.6%; Score 8; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

5 CCCTACGT 12 ઠે Sequence 2100/c

US-09-989-789-2100/c

Sequence 2100, Application US/09989769

Factoric 2100, Application US/09989769

Fatent No. 6588746

GENERAL INFORMATION:

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: POSITION OF \$11-082

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SEQ ID NO 2100

LENGTH: 9 TYPE: DNA ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-2100

28.6%; Score 8; DB 1; Length 9; 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 8; Conservative

RESULT 73 US-09-989-789-2195

Score 8.2; DB 1; Length 21; Pred. No. 1.3e+02; 0; Mismatches 3; Indels Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative

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30.0%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 51; tive 0; Mismatches 1; Indels

30.0 Best Local Similarity 90.0 Matches 9; Conservative

TYPE: DNA ORGANISM: Homo sapiens

; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)..(12) US-09-694-863-25

US-08-702-665A-19/c

Sequence 19, Application US/08702665A
Patent No. 6274708
GENERAL INFORMATION:
APPLICANT: Hilton, Douglas J.
TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CARRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza

STREET: 400 Galden City
STATE: New York
STATE: New York
CUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDEN COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,665A
FILING DATE: 20-DEC-1996
CLASSIFICATION NUMBER: 10,966
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 10,966
TELEFRANICATION NUMBER: 10,966
TELEFRANICATION INFORMATION:
TELEFRANICATION INFORMATION:
TELEFRANICATION INFORMATION:
TELEFRANICATION OF SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TTYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOINECTILE TYPE: DNA (genomic)

; MOLECULE TYPE: DNA (genomic) US-08-702-665A-19

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TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-170-095B-12
         SEQ ID NO 2454
                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2453
                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2454, Application US/09989789
Patent No. 6588746
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / S11-US2
CURRENT PAPLICATION NUMBER: US/09/989,789
CURRENT APPLICATION NUMBER: US/09/989,789
SOFTWARES FILING DATE: 2002-03-25
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2453, Application US/09989789

Patent No. 6588746

GENERAL INFORMATION:

APPLICANT: LIU, Qiana

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFRERENCE: 8325-0011.20 / S11-US2

CURRENT PILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: PATENTIN Ver. 2.0

LENGTH: 9
Sequence 2195, Application US/09989789

Patent No. 6588746

GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: PRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT PILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2195
LIENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8; DB 1; Length 9;
Pred. No. 4.1e+02;
0; Mismatches 0; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                       28.6%; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-989-789-2454/C
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US-09-989-789-2453/c
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TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
CS-09-989-789-2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: unknown to applicant MOLECULE TYPE: Other mucleic acid MOLECULE TYPE: Other nucleic acid DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE USED IN A CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CADITY BOAD TO THE STATE OF THE
                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                          28.6%; Score 8; DB 1; Le. 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.6%; Score 8; DB 1
100.0%; Pred. No. 45;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Blood Substitutes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: SOMETOGEN, Inc.
STREET: 2545 Central Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-170-095B-12; Sequence 12, Application US/08170095B; Patent No. 5563254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-396-866-12
'S-08-396-866-12', Application US/08396866
'Patent No. 5661124
                                                                                                                                                                                                                                                                                                                 100.0%; Pre
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.6
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boulder
STATE: Colorado
ZIP: 80301
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APPLICANT: Renner, Wolfgang A. APPLICANT: Renner, Wolfgang A. APPLICANT: Coberger, Georg H. APPLICANT: Orberger, Georg H. APPLICANT: Orberger, Georg H. APPLICANT: Soller, Daniel Balley, Jamiel B. TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY, TITLE OF INVENTION: ARACHERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WITITLE OF INVENTION: A REDEFERMINED PROPERTY FILE REFERENCE: 8358-0005-999
FILE REFERENCE: 8358-0005-999
FILE REFERENCE: 1998-11-17
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FeatSEQ for Windows Version 3.0
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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US-08-0410-4
; Sequence 4, Application US/08086410
; Patent No. 3407822
; Patent No. 3407822
; Patent No. 3407822
; Patent No. 3407822
; APPLICANT: LEFLATORS, Pascal
APPLICANT: SHIRE, David
; TILLE OF INVENTION: Artificial promoter for the express:
TILLE OF INVENTION: ALEADNER
STREET: Ring Street Station, Suite 500, 1800 Diagonal STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11;
                                                                                                                                                               Length 10;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,410
                                                                                                                                                               28.6%; Score 8; DB 1; 100.0%; Pred. No. 45;
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09193707
Patent No. 6524792
GENERAL INFORMATION:
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Best Local Similarity 100.0%; P.
Matches 8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               Query Match 28.6
Best Local Similarity 100.
Marches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Primer
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                                                                          US-09-301-721A-12
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Sequence 12, Application US/09301721A

APPLICANT: CHEVAL, Lydie

APPLICANT: VIELOW; Dean-Marc

APPLICANT: VIELOW; Dean-Marc

APPLICANT: VIELOW; MICROASSAY FOR SERIAL ANALYSIS OF GENE EXPRESSION AND

TITLE OF INVENTION: APPLICATION STHEROF

TITLE OF INVENTION: 1999-0X

CURRENT APPLICATION NUMBER: US/09/301,721A

CURRENT APPLICATION NUMBER: EPO 99400189.9

PRIOR FILING DATE: 1999-01-27

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 12

LENGTH: 10

TUBLE OF THE O
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GENERAL INFORMATION:

APPLICANT: Hoffman, Stephen J.
APPLICANT: Hoffman, Stephen J.
APPLICANT: Magai, Kiyoshi
TITLE OF INVENTION: Blood Substitutes
NUMBER OF SEQUENCES: 34
COMESSED SEQUENCES:
ADDRESSE: Somatogen, Inc.
STREE: 5797 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: BOADHALE FORM:
MEDIUGAT APPLE DISKELTE, 3.50 inch, 1.4 Mb storage
COMPUTER READABLE FORM:
APPLICATION TYPE: DISKELTE, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: MICCOSOFT Word 5.0a
CURRENT APPLICATION NUMBER: US/08/396,866
FILING DATE:
CRACETALING DATE:
CRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown to applicant
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE
DESCRIPTION: USED IN A CLONING VECTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,780
FILING DATE: May 17, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5661124ak, Henry P.
REGISTATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: Hoffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-441-3322
TELEPAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 8; Conserv
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0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 82
US-08-025-038-15/C
Sequence 15, Application US/08025038
Patent No. 554526
GENERALI INFORMATION:
APPLICANT: BAXTER-LOWE Lee-Ann
ITILE OF INVENTION: Method For Hila Typing
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: F01ey & Lardner
STREET: 777 E. Wisconsin Avenue
CITY: Milwaukee
STARET: Wisconsin
COMPTRE READABLE FORM:
MEDIUM TYPE: F10epy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: F10epy disk
COMPUTER: IBM PC Compatible
OMPRITING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CITRENT APPLICATION NUMBER: US/08/025,038
FILING DATE: 1993030
CLASSIFICATION NUMBER: 07/544,218
FILING DATE: 1993030
REFERENCE/DOCKET NUMBER: 204 854
TELECOMMUNICATION NUMBER: 204 854
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 12;
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28.6%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ ID NO: 15: TYPE: NUCLEIC ACID STRANDENNESS: single STRANDENNESS: linear US-08-025-038-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative 0
                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
                                                                  (703) 683-4109
                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-939-501A-17
                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 83
US-08-152-955-4
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GENERAL INFORMATION:
APPLICANT: BLAISEAU, Fierre-Louis
APPLICANT: LEGOUX, Rechard
APPLICANT: LEGOUX, Jean-Jacques
APPLICANT: SCHNEIDER, Michel
TITLE OF INVENTION: Recombinant DNA coding for a protein
TITLE OF INVENTION: Recombinant DNA coding for a protein
TITLE OF INVENTION: Recombinant DNA coding for a protein
TITLE OF INVENTION: Recombinant DNA coding for a protein
TITLE OF INVENTION: A 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LAEDNER
STREET: Road, PO Box 29
CITY: ALEXANDRIA
COUNTRY: USA
STREET: Road, PO Box 29
CONTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPAN:
APPLICATION NUMBER: FF 91 11072
APPLICATION NUMBER: FF 91 11072
ATTONNEY/AGDIT INFORMATION:
NAME: SAKE, BERTHARD
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16703)
TELECOMMUTCATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.6%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 66; tive 0; Mismatches 0; Indels
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 105 07/768,083
FILING DATE: 02-0CT-1991
APPLICATION NUMBER: FR 89 17467
FILING DATE: 29-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/318
TELEFAN: (703) 836-9300
TELEFAN: (703) 836-9300
TELEFAN: (9749)
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGHALION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
CLONE: ALBORDIA GENOMIC)
INPEDIATE SOURCE:
CLONE: CLONE: ALBORDIA L'ABBRITON FOR SEQ. CLONE: CLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-939-501A-17; Sequence 17, Application US/07939501A; Patent No. 5446138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Gaps

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Gaps
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GENERAL INCORMATION:
APPLICANT: Weiss, Arthur
APPLICANT: Weiss, Arthur
TITLE OF INVENTION: Screening Assay for the Identification
TITLE OF INVENTION: Of Immunosuppressive Drugs
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fisher & Amzel
STRRET: 1320 Harbor Bay Parkway, Suite 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 11;
                                                                                                                                                      DB 1; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 85
US-09-249-155A-272/c

| Sequence 272, Application US/09249155A |
| Sequence 272, Application US/09249155A |
| Setent No. 6538173 |
| CENERAL INFORMATION: |
| APPLICANT: Heber-Katz, Ellen |
| TITLE OF INVENTION: Compositions and Methods for Wound |
| TITLE OF INVENTION: Healing |
| TITLE OF INVENTION: Healing |
| FILE REFERENCE: 00486.78508 |
| CURRENT FILING DATE: 1999-02-13 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR PILICATION NUMBER: US 60/097,937 |
| PRIOR PILING DATE: 1998-08-26 |
| PRIOR FILING DATE: 1998-08-26 |
| PRIOR FILING DATE: 1998-09-28 |
| NUMBER OF SEQ ID NOS: 346 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 272 |
| PRIOR PILING DATE: 1998-09-28 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                           2; Indels
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                                                                                                                                                  Query Match 27.9%; Score 7.8; DB Best Local Similarity 81.8%; Pred. No. 63; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7.8; DB
Pred. No. 63;
0; Mismatches
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CITY: Alameda
STATE: California
COUNTRY: USA
ZIP: 4501
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (
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                                                                                                                                                                                                                                                                                                    18 GGGAGTCCAGG 28
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                                                  , ORGANISM: Mus musculus US-09-249-155A-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-249-155A-272
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PCT-US93-05668-4
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Sequence 4, Application US/08152955;
Patent No. 54748910;
GENERAL INFORMATION:
APPLICANT: Weiss, Arthur
APPLICANT: Praser, James
ITILE OF INVENTION: of Immunosuppressive Drugs
TITLE OF INVENTION: of Immunosuppressive Drugs
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
CITY: San Francisco
STATE: Galifornia
COUNTRY: USA
ZIP: 94105
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,955
CLASSIFICATION NUMBER: US/08/152,955
FRICK APPLICATION NUMBER: 29,541
REGISTRATION NUMBER: 29,541
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 29,541
TELERPAN: 415-326-2400
TELERPAN: 415-326-2400
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US-09-249-155A-236
Sequence 236, Application US/09249155A
Sequence 236, Application US/09249155A
Parent No. 653B173
GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILL REPERENCE: 00486, 78503
CURRENT APPLICATION NUMBER: US/09/249,155A
CURRENT APPLICATION NUMBER: US/09/249,155A
PRIOR PELING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-09-26
PRIOR APPLICATION NUMBER: US 60/102,051
PRIOR PRING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 346
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 236
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cuery Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 CAGGGAGTCCA 26
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Sequence 1007. Application US/08435350
Patent No. 5599704
GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGE
TITLE OF INVENTION: TRAIMENT OF BRE
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                      RESULT 88
US-08-435-350-107/c
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US-08-035-928-19.7

US-08-035-928-19.7

Sequence 19, Application US/08035928

Patent No. 5538844

GENERAL INFORMATION:

APPLICANT: Duvac, Mabel P.

APPLICANT: Duvac, Manes F.

APPLICANT: MacDonald, Marcy E.

APPLICANT: MacDonald, Marcy E.

APPLICANT: MacDonald, Marcy E.

TITLE OF INVENTION: A No. 553844el Transport Protein Gene from TITLE OF INVENTION: A No. 553844el Transport Protein Gene from TITLE OF INVENTION: A No. 553844el Transport Protein Gene from TITLE OF INVENTION: A No. 553844el Transport Protein Gene from TITLE OF INVENTION: A No. 553844el Transport Protein Gene from TITLE OF INVENTION: A No. 553844el Transport Protein Gene from TITLE OF INVENTION: A No. 553844el Transport Protein Gene from TITLE OF INVENTION: A No. 55384fel Transport Protein Gene from TITLE OF INVENTION OF A No. 55384fel Transport Protein Gene from STATE: 1225 Connecticut Avenue N.W.

CONDITY: Washington STATE: Do. Compatible Computible Comput
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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Pred. No. 74;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
FILING DATE: 15-JUN-1992

ATTCRNEY/AGENT INFORMATION:
NAME: Fisher, Stanley P.
REGISTRATION NUMBER: 24,344

REFERENCE/JOCKET NUMBER: 91-14

TELEPHONE: 510-748-688

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: NUCLEIC STANDEDNESS: single
TYPE: NUCLEIC STANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-05668-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.9%;
81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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US-08-494-301A-25/C
US-08-494-301A-25/C
US-08-494-301A-25/C
Sequence 25, Application US/08494301A
Sequence 25, Application US/08494301A
Sequence 25, Application US/08494301A
Sequence 25, Sequence 3cquardo
TITLE OF INVENTION: Oligonucleotides to Inhibit the
TITLE OF INVENTION: Expression of Isopremyl Protein Transferases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lucas & Ust
STREET: 205 E. 42nd Street
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 12;
                                                                                STATE: CONTRETE: USA

ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: Wordberfect (Version 5.1)
SOFTWARKE: Wordberfect (Version 5.1)
SOFTWARKE: Wordberfect (Version 5.1)
APPLICATION NUMBER: US/08/435,350
FILING DATE: AD955
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/936,531
FILING DATE: AD9125 26, 1992
ATTORNEY/AGENT NUMBER: 07/936,531
REGISTRATION NUMBER: 07/936,531
REGISTRATION NUMBER: 12,327
REFERENCE/COCKET NUMBER: 127/245
TELEPRONE (213) 955-0440
TELEPK: 67-3510
INFORMATION FOR SEQ ID NO: 107:
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%; Score 7.8;
81.8%; Pred. No. 7
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GCCCTACGTGT 14
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                    Length 12;
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                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 22314

ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,526

FILING DATE: 17-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024

REGISTRATION NUMBER: 30,024

REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/08717526

Patent No. 5786147
GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA
NUMBER OOD SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEB: OLIFF & BERRIDGE
STREET: 700 SOUTH WASHINGTON STREET
CITY: VALEXANDEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.4%; Score 7.4; DB 1;
88.9%; Pred. No. 4.1e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                       Score 7.8; DB 1;
Pred. No. 74;
1; Mismatches 2
                    CURRENT FILING DATE: 2000-03-17
EARLIER APPLICATION NUMBER: 09/223,498
EARLIER FILING DATE: 1998-12-30
EARLIER FILING DATE: 1998-12-30
EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 9
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: DNA (genomic)
US-08-717-526-61
                                                                                                                                                                                                                                                                                                       27.9%;
ilarity 72.7%;
Conservative
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Best Local Similarity 88.9.
....has 8, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                            15 ACAGGGAGICC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVAGGGAAUCC 11
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 92
US-08-717-526-61/c
                                                                                                                                                                                                                                        , ORGANISM: rat
US-09-528-404-9
                                                                                                                                                                                                                        TYPE: RNA
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Patent No. 6287769

GENERAL INFORMATION:

APPLICANT: Incue, Takakazu

APPLICANT: Incue, Takakazu

TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi

TITLE OF INVENTION: agment, Method of Assaying Contaminant

TITLE OF INVENTION: agment, Method of Assaying Contaminant

TITLE OF INVENTION: agment, Method of Assaying Contaminant

FILE REFERENCE: 9982-7

CURRENT APPLICATION NUMBER: US/09/281,418

CURRENT FILING DATE: 1999-03-30

EARLIER APPLICATION NUMBER: UF/1998/87651

EARLIER FILING DATE: 1999-03-16

SEQ ID NOS: 216

SEQ ID NOS: 216

SEQ ID NOS: 216

SED ID NOS: 216
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Patent No. 6440723
GENERAL INFORMATION:
APPLICANT: Roderic M.K. Dale
TITLE OF INVENTION: PARRAYS WITH MODIFIED OLIGONUCLECTIDE AND
TITLE OF INVENTION: POLYNUCLECTIDE COMPOSITIONS
FILE REPERENCE: OLIG-002CIP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7.8; DB
Pred. No. 74;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: 1EM 486 Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,301A
FILING DATE: 23-UUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE:
LING DATE: 29-UUNE-1994
INFORMATION POR SEQ 1D NO: 25:
BENGH: 12 Dase pairs
LENGH: 12 Dase pairs
TYPE: nuclectide
STRANDEDNESS: single
TYPE: TICHORY Inhear
ANTI-SENSE: Yes
US-08-494-301A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7.8;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Primer US-09-281-418-25
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US-09-281-418-25/c
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US-09-528-404-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.4%; Score 7.4; DB 1; Length 9; Best Local Similarity 88.9%; Pred. No. 4.1e+02; Matches 8; Conservative 0; Mismatches 1; Indels
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US-07-651-710A-33/C

Sequence 33, Application US/07651710A

Patent No. 536264

GENERAL INFORMATION:

APPLICANT: Chua. Nam-Hai

TITLE OF INVENTION: Trans-Activating Factor-1

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS: 45

CORRESPONDENCE ADDRESS: 8

ADDRESSED: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER: PLOPPY disk

COMPUTER: 1991026

CLASSIFICATION NUMBER: US/07/651,710A

FELEPHONE: APPLICATION NUMBER: 30,742

REFERENCE/DOCKET NU
US-09-153-242-30
Sequence 30, Application US/09153242
Sequence 30, Application US/09153242
BENERAL INFORMATION:
APPLICANT: Unideberg, Joakim
APPLICANT: Unideberg, Joakim
TITLE OF INVENTION: MODULAR PROBES II
FILE REFERENCE: 1181-242
CURRENT APPLICATION NUMBER: US/09/153,242
CURRENT FILING DATE: 1998-09-15
PRIOR FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECTUE TYPE: TAF-1 binding motif
US-07-651-710A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10 base paire
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGCCCTAC 10
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Jeaquence 6, Application US/08378986

Jeaquence 6, Application US/08378986

Patent No. 5723731

JEDENARI INFORMATION: Expression Motifs That Confer TITLE OF INVENTION: Expression Motifs That Confer TITLE OF INVENTION: Expression Motifs That Confer TITLE OF INVENTION: Tissue- and Developmental-Specific Expression in Plants Ornerson Programmer of Sagurances: Adoresses: Adoresses: Adoresses: Adoresses: Adoresses: Adoresses: Adoresses: Adoresses: Pomie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York, STATE: New York, COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: ADELICATION DATA: PC-DOS/NS-DOS

SOFTWARE: Perentin Release #1.0, Version #1.25

CURRENT APPLICATION NATA: B00

PRIOR APPLICATION NUMBER: US/09/982,792

FILING DATE: 30-NOV-1992

ATTORNEY/AGENT INFORMATION: NOW: NAME: Occurati, Laura A. NAME: Contai, Laura A. S. ATTORNEY/AGENT INFORMATION: NAME: CALL PENIER B. SECUENT INFORMATION: NAME: CALL PENIER B. SECUENT INFORMATION: NAME: CALL PENIER B. SECUENT INFORMATION: TELEPAX: (212) 869-8864/9741

FIREMENT: GALI PENIER B. SECUENT INFORMATION: TELEPAX: (212) B69-8864/9741

FIREMENT: LEBRANT: LINEMER: AGAIL PENIER B. SEQUENT INFORMATION: NAME: CALL PENIER B. SEQUENT INFORMATION: NAME: CAL
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                                                                                                                                                                                                                                                                             02356.0066-00000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/074,879
FILING DATE: 16-UN-1993
APPLICATION NUMBER: W0 92/1136
FILING DATE: 09-UL-1992
ATTOMACY AGENT INFORMATION:
NAME: POLLET, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERNCE/DOCKET NUMBER: 33,332
REFERNCE/DOCKET NUMBER: 30,2356,0066-(COMMAN)
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10 base pairs
TYPE: nucleic acid
TYPE: double
TOPOLOGY: unknown
MOLECULE TYPE: Opaque 2 binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 ACAGGGAGT 23
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Sequence 3, Application US/08468057A;
Parent No. 5565535;
GENERAL INFORMATION:
APPLICANT: Orth, Gerard
APPLICANT: Streek, Rolf
ITILE OF INVENTION: DNA Sequences Derived from the Genome of
ITILE OF INVENTION: the Papillomavirus HPV39, Their Use in In Vitro Diagnosis;
ITILE OF INVENTION: and for the Production of an Immunogenic Composition:
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,057A
FILLING DATE: 06-UN-1995
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,879
FILING DATE: 16-70N-1993
CLASSIFICATION: 435
FILING DATE: 16-70N-1992
ATTCRNEY/AGENT INFORMATION:
NAME: POTEN: 09-70L-1992
ATTCRNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 33,332
TELEFAX: 202-408-4400
INFORMATION: OR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LUMGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.4%; Score 7.4; DB Best Local Similarity 88.9%; Pred. No. 66; Matches 8; Conservative 0; Mismatches
                                          SEE: Dunner
: 1300 I Street, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-074-879-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 ACAGGGAGT 23
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                                                                                                                                                                          USA
                                              ADDRESSEE:
                                                                                                   CITY: Was
STATE: DC
COUNTRY:
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Gaps

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Score 7.4; DB 1; Length 10;
Pred. No. 66;
0; Mismatches 1; Indel8
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RESULT 10.

US-08-388-353-657/c

; Sequence 657, Application US/08388353
; Patent No. 6010895
; APPLICANT: Cooper, Dale A.
APPLICANT: Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STATE: Now York
COUNTRY: United States
ZIP: 11530
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DATE: 14-FEB-1995
; FLING DATE: 14-FEB-1995
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: New York
COUNTRY: United States
ZIP: 11530
COMPUTER: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: EMP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Didigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERRNE/PORTE NUMBER: 31,346
REFERRNE/PORTE NUMBER: 31,346
REFERRNE/PORTE NUMBER: 31,346
REFERRNE/PORTE NUMBER: 9606
TELECOMMUNICATION INFORMATION:
NAME: Didigilo, Frank S.
REGISTRATION FOR SEQ ID NO: 496:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNES: single
STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic) US-08-388-353-496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 ACAGGGAGT 23
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26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                    Score 7.4; DB 1; Length 10;
Pred. No. 66;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 495, Application US/08388353
Facent No. 6010855
GENERAL INFORMATION
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Nicholas J.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crower, David
APPLICANT: Crower, David
APPLICANT: Crower, David
APPLICANT: Crower, Suzanne
APPLICANT: Crower, Solot
APPLICANT: Crower, Suzanne
APPLICANT: Crower, Suzanne
APPLICANT: Crower, Suzanne
APPLICANT: Crower, Suzanne
CITY: Garden City Plaza
CITY: Garden City
STAFET: New York
COUNTRY: United States
ZIP: 11530
COMPUTER: EMP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-1995
CLASSIFICATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 496, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
) MOLECULE TYPE: DNA (genomic)
US-08-388-353-495
                                                                                        Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 ACAGGGAGT 23
                                                                                                                                                                                                                          7 CTACGTGTA 15
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                               US-08-378-986-6
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Best Local Similarity 88.9%; Fred. No. 66; Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 658, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION
APPLICANT: Deacon, Nicholas J.
APPLICANT: Carmont, Jennifer C.
APPLICANT: Crowe, Suzane
APPLICANT: Crowe, Suzane
TITLE OF INVENTION: NO.PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: L153.

COMPUTER: TEMPOR disk

MEDIUM TYPE: Floppy disk

COMPUTER: TEM PC Compatible

COMPUTER: TEM PC COMPATIBLE

COMPUTER: TEM PC COMPATIBLE

COMPUTER: TEM PC COMPATIBLE

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NOMBER: US/08/388,353

FILING DATE: 14-FEB-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: DIGGLIO, FRANK S.

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 9606

TELECHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.4%; Score 7.4; DB Best Local Similarity 88.9%; Pred. No. 66; Matches 8; Conservative 0; Mismatches
                                                                                                TELEYA: (516) 742-4343
TELEYA: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 657:
SEQUENCE CHARACTERISTICS:
TVOE
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: DiGIGLIO, Frank 31,346
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 960
TELECOMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                               , MOLECULE TYPE: DNA (genomic)
US-08-388-353-657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOX SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 DASS pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: United States
                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 GTACAGGGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GTACAGGCA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11530
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Length 10;

26.4%; Score 7.4; DB 1;

Query Match

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                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Deacon, Nicholas J.

APPLICANT: Learmont, Jennifer C.

APPLICANT: McPhee, Dale A.

APPLICANT: Crowe, Susanne

APPLICANT: Crowe, Susanne

APPLICANT: Crowe, Susanne

APPLICANT: Crowe, Susanne

APPLICANT: Copper, David

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 800

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: Now York

COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United Course 21F: 11530

COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: PIBM PC COMPATIBLE COMPATIBLE FORM:
COMPUTER: PARAMETER: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: 14-FEB-1995

FILING DATE: 14-FEB-1995

CLASSIFICATION NUMBER: 31,346

ATTORNEY/AGENT INFORMATION:
NAME: DidGATION NUMBER: 3666

TELERBANCE/DOCKET NUMBER: 3666

TELERBANCE/DOCKET NUMBER: 3666

TELERBANCE (516) 742-4343

TELEBRAX: (516) 742-4346

TELEBRAX: (516) 742-4366

TELEBRAX: (516) 742-4366

TELEBRAX: (510) NO: 661: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dearmont, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 662, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
                                                                                                                                                                                     Sequence 661, Application US/08388353
Patent No. 6010895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.8
Matches 8; Conservative
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13 GTACAGGGA 21
                                                 9 GTACAGGCA 1
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STRANDEDNESS: sin
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Patent No. 601566

GENERAL INFORMATION:

APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TILLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SIQUENCES: 841
CORRESPONDENCE ADDRESS:

GITY: GRADEN CITY PLAZA
COUNTRY: US.A.
STREE: NEW YORK
COUNTRY: US.A.
ZIF: 11530-0239
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: OF TOOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 11-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 11-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
APPLICATION NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.4%; Score 7.4; DB 1; Best Local Similarity 88.9%; Pred. No. 66; Matches 8; Conservative 0; Mismatches 1
                                                                           US 08/388,353
                               FILING DATE: 23-DEC-1994

**PLICATION NUMBER: US 08/386

**PLING DATE: 14-FEB-1995

**APPLICATION NUMBER: PN3021/95

**FILING DATE: 17-NAY-1995

**ATTORNEY AGENT INFORMATION:
NAME: PRANK S. DIGIGILO:
REPERENCE/DOCKET NUMBER: 9606

**TELECOMUTUNICATION INFORMATION:
TELEFAN: (516) 742-4343

**TELEFAN: (516) 742-4343

**TELEFAN: (516) 742-4366

INFORMATION FOR SEQ ID NO: 495:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: NUCLEIC TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 ACAGGGAGT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-488-551B-496/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-488-551B-495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7.4; DB 1; Length 10;
Pred. No. 66;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
CITY:
CITY:
CITY:
COMPUTE:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER:
C
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEB: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: DNA (genomic)
US-08-388-353-662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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Pred. No. 66;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                       26.4%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 66; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Nicholas J. Deacon
APPLICANT: Nicholas J. Deacon
APPLICANT: Noichee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: ORADBO CITY
STATE: NEW YORK
COUNTRY: US.A.
ZIP: 11530-0299
COMPUTER: IBM PC compatible
OFERATING SYSTEM: POOP/MS-DOS
SOFTWARE: PACHAIN Release #1.0, Version #1.25
COMPUTER: IBM PC compatible
OFERATING SYSTEM: US/08/488,551B
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 11-FEB-1994
APPLICATION NUMBER: PM3021/95
FILING DATE: 11-FEB-1995
APPLICATION NUMBER: US/08/353
FILING DATE: 11-FEB-1995
APPLICATION NUMBER: US/08/389,353
FILING DATE: US/08/389,353
FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-08-488-551B-657/c
Sequence 657, Application US/08488551B
Setent No. 6015661
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative (
                                                                                                                                                                                                              10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                15 ACAGGGAGT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: DNA
US-08-488-551B-657
                                                                                            ACLOGY: linear

MOLECULE TYPE: DNA

US-08-488-551B-496
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                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DaleA. McPhee
APPLICANT: DaleA. McPhee
APPLICANT: David Cooper
ITILE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & FRESSER
STRATE: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
CITY: GARDEN CITY
COUNTRY: U.S. A.
ZIP: 11530-0229
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: PARABLE FORM:
MEDIUM TYPE: PROPEY disk
COMPUTER: DAPLICATION DATA:
APPLICATION NUMBER: W1806 (AU)
FILING DATE: 07-UN-1995
FRIING DATE: 11-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM302 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM302 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM302 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM302 (AU)
FILING DATE: 17-MAY-1995
FILING DATE: 17-MAY-1995
ATTOME FRANK S. DIGIGIO
REFERENCE/DOCKET NUMBER: PM302 (AU)
FILING DATE: 17-MAY-1995
ATTOME FRANK S. DIGIGIO
REFERENCE/DOCKET NUMBER: PM302 (AU)
FILING DATE: 17-MAY-1995
ATTOME FRANK S. DIGIGIO
REFERENCE/DOCKET NUMBER: PM302 (AU)
FILING DATE: 17-MAY-1995
ATTOME FRANK S. DIGIGIO
REFERENCE/DOCKET NUMBER: PM302 (AU)
FILING DATE: 17-4-4366
INFORMATION FOR SEQ ID NO: 658:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
LENDER THE TOWEN THE PM TERESPONE
TERESPONE THE PM TERESPONE
TERESPONE THE TERESPONE
TERES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-488-551B-661
; Sequence 661, Application US/08488551B
; Patent No. 6015661
; Patent No. 6015670:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: David Cooper
; APPLICANT: David Cooper
; APPLICANT: David Non-PATHOGENIC STRAINS OF HIV-1;
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 66;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.4%; Score 7.4;
RESULT 108
US-08-488-551B-658/c
; Sequence 658, Application US/08488551B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
26.4
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 GTACAGGGA 21
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US-08-488-5518-658
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Gaps

13 GTACAGGGA 21

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Gaps
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Sequence 813, Application US/08488551B
Patent No. 6015661

GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER: DEAPCABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: PROPER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-UUN-1995
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM028 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM028 (AU)
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: PM028 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.4%; Score 7.4; DB
88.9%; Pred. No. 66;
tive 0; Mismatches
  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,551B
FILING DATE: O7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-FEB-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT THORMATION:
NAME: FRANK S. DIGIGIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPXX: (516) 742-4343
INFORMATION FOR SEQ ID NO: 662:
SEQUENCE: CHARACTERISTICS:
LENGTH: 10 base pairs
TUNDER: NUMBER: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 TGTACAGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-488-551B-662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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US-08-488-551B-662

Sequence 662, Application US/08488551B
Patent No. 601561
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TITLE OF INVENTION:
NON-PATHOGENIC STRAINS OF HIV-1
TITLE OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GANDEN CITY PLAZA
CITY: GARDEN CITY
COUNTRY: U S.A.
ZIP: 11530-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentTn PC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GANDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUW TYEE: CIOPOPY disk
COMPUTER READABLE FORM:
MEDIUW TYEE: CIOPOPY disk
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 07-UW1-1995
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-DEC-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-DEC-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
TELEFRAX: (516) 742-4366
INFORMATION POR SEQ ID NO: 661:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TUBNGTH: 10 base pairs
TUBNGTH: 10 base pairs
TUBNGTH: 11 base pairs
TUBNGTH: 11 base pairs
TUBNGTH: 11 base pairs
TOPOLOGY: linear
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26.4%; Score 7.4; DB
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-661
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APPLICANT: King Dr., David G.
APPLICANT: King Dr., David J.
APPLICANT: King Dr., David J.
APPLICANT: Wentura, Daniel A.
APPLICANT: Wentura, Daniel A.
APPLICANT: Brasis Dr., Allan R.
APPLICANT: Brasis Dr., Allan R.
APPLICANT: Brasis Dr., Allan R.
TITLE OF INVENTION: Combinatorial Selection of Phosphothionate
ITLE REFERENCE: 122144-1005
FILE REFERENCE: 122144-1005
CURRENT APPLICATION NUMBER: 60/9425,798A
CURRENT FILING DATE: 1999-10-25
PRIOR PLING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                        US-08-522-384-34/c
; Sequence 34, Application US/08522384
; Sequence 34, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: LOPEZ-NIETO, CARLOS E
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-44029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT APPLICATION NUMBER: US/08/522,384
; NUMBER OF SEQ ID NAS: 122
; SOFTWARE: PATENTIN Ver. 2.1
; ENGLID NO 34
; FEMATOR: 10
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* OTHER INFORMATION: Description of Artificial Sequence: aptamer
US-09-425-798-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.4%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 66; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Unknown Organism: Primer US-08-522-384-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7.4; DB 1; Length 10;
Pred. No. 66;
0; Mismatches 1; Indels
                                                                                         26.4%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 66;
                                                                                                                                                0; Mismatches
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; Sequence 12, Application US/09425798A
; Patent No. 6423493
; GENERAL INFORMATION;
; APPLICANT: Gorenstein Dr., David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Unknown Organism
                                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                     15 ACAGGGAGT 23
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           ; MOLECULE TYPE: DNA
US-08-488-551B-814
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LENGTH: 10
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Fatent No. 601561
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY
CATT. GARDEN CITY
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: GARDEN CLIX
STATE: NEW YORK
COUNTRY: U.S.A.

ZURTE: NEW YORK
COUNTER: U.S.A.

ZURP: 11530-0299
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPA:
MEDICATION DATA:
APPLICATION NUMBER: US/08/486,51B
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM364 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: BN0284 (AU)
FILING DATE: 12-FEB-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 12-FEB-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 17-AAY-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 17-AAY-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 17-AAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANKE/POCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 814:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
26.4%; Score 7.4; Di
Best Local Similarity 88.9%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches
PTLING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGILO:
REFERENCE/DOCKET NUMBER: 9606
TELECOMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4343
INFORMATION FOR SEQ ID NO: 813:
SEQUENCE FRANCES SEQ ID NO: 813:
TENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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STRANDEDNESS: single
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US-08-488-551B-813
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Sequence 27, Application US/09301721A

Sequence 27, Application US/09301721A

Sequence 27, Application US/09301721A

Sequence 27, Application US/09301721A

GENERAL INFORMATION:

APPLICANT: CHANAL, Ugain

APPLICANT: ELALOUF, Jean-Marc

APPLICANT: VIRLON, Berangere

TITLE OF INVENTION: APPLICATIONS THEREOF

FILE REFERENCE: 0846-0499-0X

CURRENT APPLICATION NUMBER: US/09/301,721A

CURRENT APPLICATION NUMBER: EPO 99400189.5

PRIOR PILING DATE: 1999-01-27

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 27

LENGTH: 10
                                                               APPLICANT: Wade, Nicholas M.
APPLICANT: Harrison, Bruce T.
APPLICANT: Harrison, Bruce T.
APPLICANT: APPLICANT: ALIGH BELIAN W.
APPLICANT: Reed, Kenneth C.
APPLICANT: Murphy, Kathleen M.
TILLE OF INVENTION: ANALYSIS OF Y-CHRONOSOMAL DNA SEQUENCES
TITLE OF INVENTION: ANALYSIS OF Y-CHRONOSOMAL DNA SEQUENCES
FILE REFREENCE: Wade et al
CURRENT FILLIG DATE: 2000-03-22
FRICA APPLICATION NUMBER: P07802
PRICA FILLING DATE: 1997-07-09
PRICA PLLING DATE: 1998-07-09
PRICA FILLING DATE: 1998-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA
US-09-301-721A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7.4; DB 1; Length 10; Pred, No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.4%; Score 7.4; DB 1; Length 10; B8.9%; Pred. No. 66;
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; Sequence 160, Application US/09508753B
? Eatent No. 6544736
; GENERAL INFORMATION:
Sequence 26, Application US/09462561B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Equus caballus
US-09-462-561B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GTACAGGGA 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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Pred. No. 66;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.4%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 66; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-154-750A-37
Sequence 37, Application US/09154750A
Sequence 37, Application US/09154750A
Sequence 37, Application US/09154750A
Selent No. 6412640
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: 1953-Induced Apoptosis
FITLE OF INVENTION: 1953-Induced Apoptosis
FITLE OF INVENTION: 1953-Induced Apoptosis
FITLE APPLICATION NUMBER: 090/154,750A
CURRENT PILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/059,153
FRIOR APPLICATION NUMBER: 60/059,153
FRIOR FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEGOTUMARE: FastSEQ for Windows Version 3.0
                                                                                                                               US-09-154-750A-17/c

Sequence 17, Application US/09154750A

Sequence 17, Application US/09154750A

Sequence 17, Application US/09154750A

GENERAL INFORMATION:
APPLICANT: Vegelstein, Bert
APPLICANT: FOLYAK, Kornelia

TILE CO INVENTION: P53-Induced Apoptosis
FILE REFERENCE: 1107, 753-7

CURRENT FILING DATE: 1998-09-17

PRIOR PILING DATE: 1998-09-17

PRIOR PILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-03-30

NUMBER OF SEQ ID NOS: 93

SOFTWARE: FEASED for Windows Version 3.0

SEQ ID NO: 17
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-09-154-750A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-17
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  10 CGTGTACAG 18
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                                           10 CATGTACAG
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Matches 8; Conserv
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US-09-462-561B-26/c

RESULT 117

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17 AGGGAGTCC 25
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US-09-989-789-1630
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LENGTH: 10
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APPLICANT: SRIVASTANA, SHIV

APPLICANT: MOUL, UDDD W.

APPLICANT: MOUL, UDDD W.

APPLICANT: MOUL, UDDD W.

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: PROSTATE-SOUGOO-

CURRENT APPLICATION NUMBER: US/09/769,482

CURRENT FILING DATE: 2000-01-26

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PALENTIN VAIL 2.1

SEQ ID NO 18

LENGTH: 10
Yasuhiro FURUICHI

Yasuhiro FURUICHI

Yuko SHIBATA

APPLICANT: Hiroko FUNAKI

APPLICANT: Hiroko FUNAKI

APPLICANT: Hiroko FUNAKI

TITLE OF INVENTION: MATAHIKI

TITLE OF INVENTION: MATOH for Synthesizing cDNA from mRNA sample

FURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT APPLICATION NUMBER: US/09/508,753B

PRIOR FILING DATE: 1997-09-18

NUMBER OF SEQ ID NOS: 472

LENGTH: 10

TYPE: NV-
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US-09-769-482-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.4%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 66; Matches 8; Conservative 0; Mismatches 1; Indels
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88.9%; Pred. No. 66;
tive 0; Mismatches
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US-09-504-132-10/c
; Sequence 10, Application US/09504132
; Betent No. 6582899
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 120
US-09-769-4812-18/C
Sequence 18, Application US/09769482
Patent No. 6566130
GENERAL INFORMATION...
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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"LICANT: Kamb, Carl Alexander

"TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS THAT CAUSE A LETHAL

"TITLE OF INVENTION: PHENOTYPE, AND AGENTS THEREOF

"TITLE OF INVENTION: DAYS. 2000-02-15

"UNMER OF SEQ ID NOS: 26

"SEQ ID NO 10

"TYPE. ...

"TYPE. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1630, Application US/09989789

Patent No. 6588746

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILLE REPRENENCE: 8325-0011.20 / 811-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT PILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SEQ ID NO 1630

LENGTH: 10
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Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
TITLE OF LINGENTION: UNMER: US/09/989,789
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: Aptamer 4
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Pred. No. 66;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7.4; DB 1; Length 10;
Pred. No. 66;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative (
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; TYPE: DNA; ORGANISM: Artificial Sequence; PEATURE; ; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-1631
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bowman, Cludy G.
APPLICANT: Dawson, Cludy G.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Darce, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: SYNTHETIC DNA SEQUENCES PURBERS OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 SKyline Drive
                                                                                                                                                                              Query Match 26.4%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 66; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENY APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION NUMBER: US/07/951,715A
FILING DATE: MADEAN:
APPLICATION NUMBER: US/07/72,027
FILING DATE: US/07/72,027
FILING DATE: US/07/72,027
ATORNEY/AGENT INFORMATION:
NAME: SPUILIL, WHINER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
RETERRENCE/DOCKET NUMBER: S-1943
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAKE: (919) 541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/07951715A
Patent No. S625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desal, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rothstein, Steven J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crossland, Lyle D. Wright, Martha S. Merlin, Ellis J. Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
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SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 7 Skyline
CITY: Hawthorne
STATE: New York
COUNTRY: USA
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Gaps
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                                                               DB 1; Length 11;
                                                                                       1; Indels
), DESCRIPTION: /desc = "primer for third quarter

), DESCRIPTION: first half"

') HYPOTHETICAL: NO

US-07-951-715A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-UUN-1995
CLASSITCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY, AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REGISTRATION NUMBER: GG 1577/CIP/DIV4
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: (19) 54-18582
                                                             Score 7.4; DB
Pred. No. 80;
0; Mismatches
                                                                                                                                                                              RESULT 125
US-08-459-448A-55/c
; Sequence 55, Application US/08459448A
; Detent No. 585934
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
                                                                                                                                                                                                                                            Koziel, Michael G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (919) 541-8689
                                                               Query Match
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Butcie, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: SYNTHETIC DNA SEQUENCES, 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Rd., POB 2005
CITY: Tairyfown
STREET: Rd., POB 2005
CITY: Tairyfown
STREET: New York
COUNTRY: USA
                                                                                                                                                                                                                                              .
0
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26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING APPLICATION DATA:
ATTORNEY AGENT INFORMATION:
NAME: Pace, Gary M
REGISTRATION NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
NAME: Pace, Gary M
TELECOMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer for third quarter
DESCRIPTION: first half"
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 55, Application US/08459595A Patent No. 6018104 GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kramer, Vance C.
Warren, Gregory W.
Bvola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (919)541-8582
(19)541-8689
                                                                                                                                                                                                                                                                                               14 TACAGGGAG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-459-595A-55/c
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TYPE: MINISTERS: single

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DESCRIPTION: /desc = "primer for third quarter
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CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
                                                                                                                   Score 7.4; DB
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
                                                                                                                                                             0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
JLE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (919)541-8587
TELEPRA: (919)541-8689
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        US-09-547-422-55/c
; Sequence 55, Application US/09547422
; Patent No. 6220100
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                     Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                          14 TACAGGGAG 22
                                                                                                                                                                                                                                                      11 TACAGGGG 3
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CORRESPONDENCE PUDRESS:
ADDRESSE: No. 6121014artis Agribusiness Biotechnology Research, Inc. STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: NC. 5TATE: NC. COUNTRY: USA
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT ROZIEL, Michael G.
APPLICANT ROZIEL, Malini M.
Desai, Nalini M.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 02-Jun-1995
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                         26.4%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                     1; Indels
                                                                             STANDEDNESS: SIGGL

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

BESCRIPTION: /desc = "primer for third quarter;

HYPOTHETICAL: NO

US-08-459-504B-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-8F8-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 55, Application US/08459444A Patent No. 6121014 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INPORMATION TELEPRONE: (919)541-8887 TELEPRAX: (919)541-8689 INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                  SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  14 TACAGGGAG 22
                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                          11 TACAGGGG 3
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CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6320100artis Agribusiness Biotechnology Research, Inc. STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
SIATE: NC
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crosland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Laulis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                        ö
                                                                                                                                      1; Length 11;
                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
MOLECULE TYPE: other nucleic acid
BESCRIPTION: /desc = "primer for third quarter;
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-08-459-444-55
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US-09-249-155A-203/c
; Sequence 203, Application US/09249155A
; Patent No. 6538173
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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US-09-249-155A-203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 GTACAGGGA 21
11 GTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GTCCAGGGA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                  US-09-249-155A-162
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                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.4%; Score 7.4; DB 1; Length 11; Best Local Similarity 88.9%; Pred. No. 80; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 61, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
    APPLICANT: Hober Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR PILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
                                      DB 1; Length 11;
                                                                               1; Indels
                                      Score 7.4; DB Pred. No. 80; 0; Mismatches
                                                                                                                                                                                                                                                                                       | Falent No. 0.40294
| Falent No. 0.40294
| APPLICANT: Lundeberg, Joakim |
| APPLICANT: Lundeberg, Joakim |
| APPLICANT: Lundeberg, Joakim |
| TITLE OF INVENTION: McDular PROBES II |
| TITLE REFERENCE: 1181-242 |
| CURRENT FILING DATE: 1999-09-15 |
| PRIOR PILING DATE: 1997-09-26 |
| NUMBER OF SEQ ID NOS: 63 |
| SOFTWARE: PatentIN Ver. 2.1 |
| SEQ ID NO 29 |
| LENGTH: 11
                                                                                                                                                                                                                                                         Sequence 29, Application US/09153242
Patent No. 6482592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                      Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
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                                                                                                                    14 TACAGGGAG 22
                                                                                                                                                        11 TACAGGGG 3
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US-09-249-155A-61/c
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US-09-153-242-29
US-09-547-422-55
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Pred. No. 80;
0; Mismatches 1; Indels
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| Sequence 162, Application US/09249155A |
| Sequence 162, Application US/09249155A |
| Patent No. 6538173 |
| GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT; Heber-Katz, Ellen |
| TITLE OF INVENTION: Compositions and Methods for Wound |
| TITLE OF INVENTION: Compositions and Methods for Wound |
| TITLE OF INVENTION: GENERAL ELING DATE: 1999-02-12 |
| CURRENT APPLICATION NUMBER: US 60/074,737 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-08-26 |
| PRIOR APPLICATION NUMBER: US 60/102,051 |
| PRIOR PILING DATE: 1998-08-26 |
| PRIOR PILING DATE: 1998-08-26 |
| PRIOR PILING DATE: 1998-08-26 |
| NUMBER OF SEQ ID NOS: 346 |
| SEQ ID NO ISSO ID NOS: 346 |
| SEQ ID NO ID NO ISSO ID NOS: 346 |
| SEG ID NO ID NO ISSO ID NOS: 346 |
| SEG ID NO ID NO ISSO ID NOS: 346 |
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| SEG ID NOS ISSO ID NOS: 346 |
| SEG ID NOS ISSO ID NOS ISSO ID NOS ID NOS
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APPLICANT: Heber-Katz, Ellen
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILE REFERENCE: 00486.78503
CURRENT FILING DATE: 1999-02-13
PRIOR PRILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-08-26
PRIOR FILING DATE: 1998-08-26
PRIOR FILING DATE: 1998-08-26
PRIOR FILING DATE: 1998-09-38
NUMBER OF SEQ IO NOWER: 346
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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88.9%; Pred. No. 80;
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APPLICANT: Barrett, Graham L
TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULIY, SCOCT, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
COUNTRY: U.S.A.
ZIP: ILS30
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: CONFOURE: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,792A
FILING DATE: 18-OCT-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/COCKET NUMBER: 3
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NS-09-249-155A-231/C
| Sequence 231, Application US/09249155A
| Sequence 231, Application US/09249155A
| Patent No. 65.817N-1
| GENERAL INFORMATION:
| TILE OF INVENTION: Compositions and Methods for Wound
| TILE OF INVENTION: Healing
| FILE REFERENCE: 00466.7860.
| FILE REFERENCE: 00466.7860.
| FILE REPERENCE: 00466.7860.
| FILE OF INVENTION: Healing
| FILE REPERENCE: 0046.7860.
| FRICH APPLICATION NUMBER: US 60/094,737
| PRIOR FILING DATE: 1998-09-13
| PRIOR FILING DATE: 1998-09-28
| PRIOR APPLICATION NUMBER: US 60/097,937
| PRIOR PRIOR TILING DATE: 1998-09-28
| NUMBER OF SEQ ID NOS: 346
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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88.9%; Pred. No. 80;
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Patent No. 5837694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Mus musculus
US-09-249-155A-231
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                                                                                                                                                                                                                                           Query Match
26.4%; Score 7.4; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 6; Indels
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DESCRIPTION: /desc = "DNA oligonucleotide"
TYPE: nucleic acid
STRANDEDNESS: single
FOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA oligonucleotide"
US-08-631-792A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:

PRIOR APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/633,792

FILING DATE: 01-JUL-1996

APPLICATION NUMBER: AU PM/1870

FILING DATE: 18-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Diddiglio, Frank S.

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 10062

TELECHMUNICATION NUMBER: 10062

TELEPHONE: 616)742-4343

TELEFAX: 616)742-4343

TELEFAX: 616)742-4366

TELEFAX: 616)742-4366

TELEFAX: 616)742-4366

TELEFAX: 19 010 SANS UR

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE INCLES CAID

TYPE CAID
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Best Local Similarity
Matches 11; Conserva
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US-09-075-717A-6
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LENGTH: 11 base pairs
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Sequence 35, Application US/08531137B

Sequence 35, Application US/08531137B

Sequence 35, Application US/08531137B

Sequence 35, Application US/08531137B

THE OF INVENTION: Computer-Aided Visualization and TITLE OF INVENTION: Analysis System for Sequence Bvaluation TITLE OF INVENTION: Analysis System for Sequence Bvaluation WOMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS: ATTER, Van Pelt & Yi LLP

STREET: 4906 El Camino Real, Suite 205

CITY: Los Altos

STREET: California
Sequence 35, Application US/08327525A
; Sequence 35, Application US/08327525A
; Sequence 35, Application US/08327525A
; Parent No. 57957H
; GENERAL INFORMATION:
APPLICANT: Ward, Chunwei
; APPLICANT: Bernhart, Derek H.
APPLICANT: Bernhart, Derek H.
APPLICANT: Lasohurz, Robert J.
TILLE OF INVENTION: Analysis System for Sequence Evaluation
; TILLE OF INVENTION: Analysis System for Sequence Evaluation
; TILLE OF INVENTION: Analysis System for Sequence Evaluation
; CARRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STAREE: California;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco STATE: California (COUNTRY: USA ZIP: 94111-3834

CONDUTER READABLE FORM: MEDIUM TYPE: FIDOPY disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/327,525A FILING DATE: OGCODER 21, 1994

ATTORNEY/AGENT INPORMATION: 435

ATTORNEY/AGENT INPORMATION: REGISTRATION NUMBER: 32,483

REGISTRATION NUMBER: 32,483

REGISTRATION NUMBER: 32,483

RELEEPAN: 415-326-2400

TELEPAN: 415-326-2420

TELEPAN: 415-326-2420

TELEPAN: 415-326-2420

TELEPAN: 415-326-3400

TELEPAN: 415-326-3400

TELEPAN: 415-326-3400

TELEPAN: 415-326-3400

TELEPAN: 415-326-3400

TELEPAN: 415-326-3400

TYPE: NUCLEA COUNTRY ON SEQ ID NO: 35: SEQUENCE CHARACTERISTICS: LENGTH: 11 base pairs TYPE: NUCLEA COUNTRY SEQ ID NO: STANDEDNESS SINGLE STANDEDNESS SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.7%; Score 7.2; DB Best Local Similarity 75.0%; Pred. No. 90; Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 ACAGGGAG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-327-525A-35
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WEDION TYPE: Floppy disk

COMBUTER: Tabk Proceedable DS

COMBUTER: Tabk Procedable DS

SORDWARD ABLICATION NUMBER 18 10, Version #1.25

COMBUTER: October 16, 1995

TATANSET APPLICATION NUMBER 18 10, 1995

TATANSET APPLICATION NUMBER 18 10, 1995

ATTORNEY/AGENT INFORMATION:

FREEDROWS FOOTON NUMBER 18 10, 1995

ATTORNEY/AGENT NUMBER 18 10, 1995

ATTORNEY/AGENT NUMBER 18 10, 1995

FREEDROWS FOOTON NUMBER 18 10, 1995

TREEDROWS 609 100 100 33:

SEQUENCE TARRESHOWS FOOTON NUMBER 18 10, 1995

TREEDROWS 609 100 100 33:

SEQUENCE TAYER DNA (Oldgomuclectide)

TREEDROWS 609 100 NO 33:

SEQUENCE TAYER NUMBER 18 10, 1996

TREEDROWS 100 NO 33:

SEQUENCE TAYER NUMBER 18 10, 100 1; Length 11;

DARREST 1778: DNA (Oldgomuclectide)

ON TREEDROWS 18 10 NO 1990

AND 11 ACAGORA 22

DISCOURTED NUMBER 18 10, 100 1; Length 11;

DARREST NUMBER 18 10, 100 10, 100 1; Length 11;

DARREST NUMBER 18 10, 100 10, 100 1; Length 11;

DARREST NUMBER 18 10, 100 10, 100 10, 100 10, 100 1; Length 11;

DARREST NUMBER 18 10, 100 10, 100 10, 100 10, 100 1; Length 11;

DARREST NUMBER 18 10, 100 10, 100 10, 100 1; Length 11; Length 11;
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FEATURE:
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US-09-796-071-35
; Sequence 35, Application US/09796071
; Patent No. 6607887
; GENERAL INFORMATION:
; GENERAL TROCKMATION:
; TITLE OF INVENTION: Computer-Aided Visualization and
TITLE OF INVENTION: Analysis System for Sequence Evaluation
                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6607887

"NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: ALLOS ALLOS
CORRESPONDENCE ADDRESS:
ADDRESSE: Ritter, Van Pelt & Yi LLP
STREET: 4906 El Camino Real, Suite 205
CITY: Los Altos
STREET: California
COUNTRY: USP GEL Camino Real, Suite 205
ZIP: 94022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTER: PC-000/MS-DOS
SOFTWARE: PROFICE TOOP MAR.
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/796,071
FILING DATE: 27-Feb-2001
CLASSIFICATION NUMBER: 08/531,137
ATTORISY/AGBNT INFORMATION:
NAME: Ritter, Michael J.
REGISTRATION NUMBER: 36,653
REFISENCE/DOCKET NUMBER: 36,653
REFISENCE/DOCKET NUMBER: 36,653
REFISENCE/DOCKET NUMBER: AFFYPO06
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: 650-903-1500
                                                                                                                                            .
0
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25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                           Score 7.2; DB 1; Length 11;
Pred. No. 90;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;

MOLECULE TYPE: DNA (oligonucleotide);

SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-796-071-35
                      ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
V5-019-158-765-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 141
US-09-281-418-107
; Sequence 107, Application US/09281418
; Patent No. 6287769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ 1D NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                               Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 ACAGGGAG 22
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Sequence 25. Application US/09281418
| Sequence 25. Application US/09281418
| Patent NO. 628769
| GENERAL INFORMATION:
| APPLICANT: Inoue, Takakazu
| TITLE OF INVENTION: Method of Assaying Microorganisms, Method of Assaying Microorganisms, Method of Analyzing N
| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
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| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
| TITLE OF INVENTION: nisms and Method of Assaying Contaminant
| TITLE OF INVENTION
APPLICANT: Inoue, Takakazu

TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA
TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing N
TITLE OF INVENTION: nisms and Method of Assaying Microorganisms, Method of Analyzing N
TITLE OF INVENTION: nisms and Method of Assaying Contaminant
FILE REFERENCE: 9982-7
CURRENT APPLICATION NUMBER: US/09/281,418
CURRENT FILING DATE: 1999-03-30
EARLIER FILING DATE: 1999-03-31
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 216
SEQ ID NO 107
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gabe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 16+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7.2; DB 1;
Pred. No. 1e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 297, Application US/08182968A
Patent No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.v
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 TGTACAGGGAGT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 143
US-08-182-968A-297/c
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APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/982,968
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WATCHDURG, RICHARD 1
REGISTRATION NUMBER: 32,327
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 297:
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 ACAGGGAGTCCA 26
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 Accredacreca 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-08-774-306A-297
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US-08-774-306A-297/C

Sequence 297, Application US/08774306A

Patent No. 5869253

GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.

TITLE OF INVENTION: METHOD AND REAGENT FOR

TITLE OF INVENTION: UNIUS REPLICATION

NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STREET: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: Storage

COMPUTER: IEM Compatible

COMPUTER: IEM Compatible

COMPUTER: IEM Compatible

COMPUTER: MEDIUM TYPE: STORAGE

COMPUTER: MEDIUM TYPE: STORAGE

COMPUTER: NOT Perfect 5.1

CURRENT APPLICATION DATA:

SOFTWARE: UCCHAIN

SOFTWARE: UCCHAIN

SOFTWARE: UCCHAIN

SOFTWARE: WORD PAFFECT 5.1

CURRENT APPLICATION DATA:

FILING DATE: December 26, 1996
                                                                                                       CITY: Los Angeles
STREET: SULTE 4,00
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
APPLICATION NUMBER: U$/08/1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 205/277
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 ACAGGGAGTCCA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY:
US-08-182-968A-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 ACCTGGACTCCA 2
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
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Query Match 25.7%; Score 7.2; DB 1; Length 15; Best Local Similarity 75.0%; Pred. No. 1.4e+02; Matches 9; Conservative 0; Mismatches 3; Indels
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US-09-064-156A-297/c
; Sequence 297, Application US/09064156A
; Patent No. 612966
; GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 498
CORRESPENDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIL:
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER: 18 5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
MERATION NUMBER: 18/09/064,156A
PRILING DATE: APPLICATION NUMBER: 08/174,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: MAY 14, 1992
ATTONNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTATION NUMBER: 23,47083
TELECOMMUNICATION INFORMATION:
TOTAL TOTAL
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RESULT 147
US-08-859-954-289/c
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Patent No. 6083695

CENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul B.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 MCKINNEY, Suite 5100
                                                                                                                                                 Score 7.2; DB 1; Length 15; Pred. No. 1.4e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.0%; Score 7; DB 1; Length 8; 100.0%; Pred. No. 4.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Houston

STATE: Texas

CONTRY: U.S.A.

ZIP: 7710-3095

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION:

APPLICATION:

PRIOR APPLICATION:

APPLICATION:

APPLICATION:

PRIOR APPLICATION:

ATT NOT APPLICATION UNMBER: 08/632,782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELEPHONE: 713/651-525
TELEPHONE: 713/651-526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "olgionucle
                                                                                                                                              Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.0
Best Local Similarity 100.
Matches 7; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                 15 ACAGGGAGTCCA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                       ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-064-156A-297
                                                                                                                                                                                                                                                                           13 ACCTGGACTCCA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-859-954-179
                                                                                                                                                                                                                                                                                                                                                             -08-859-954-179
                    LENGTH:
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20 GAGTCCA 26 ||||||| 1 GAGTCCA 7

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Patent No. 608365
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1301 MCKinney, Suite 5100
Sequence 289, Application US/08859954

Parent No. 6083635

PAPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul E.
ITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 8; 4.6e+02;
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STRATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER PREADALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER PREADALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER PREADALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER PROPERTION NUMBER: US/08/659,954
FILING DATE:
MAPLICATION NUMBER: US/08/659,954
FILING DATE:
ATPORNEY/AGENT INFORMATION:
MANTE: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REPERBENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION HORDAMATION:
TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; DB 1; Pred. No. 4.6 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.0%;
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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HYPOTHETICAL: XE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 148
US-08-859-954-436
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21 AGTCCAG 27
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US-08-859-954-510/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ठ
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Sequence 437, Application US/0885954

GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Paul E.
ITILE OF INVENTION: Gene Sequencing and Method Thereof
VUMBER OF SEQUENCES: S66
CORRESPONDENCES: S66
CORRESPONDENCES: S66
CORRESPONDENCES: S66
CORRESPONDENCES: ADDRIGH & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIF: 77010-3095
COMPUTER: ERDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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CITY: hc..

STATE: Taxas

COUNTRY: U.S.A.

ZIP: 77010-31095

COMPUTER: TEADABLE FROM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMDAIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFRENCE/DOCKET NUMBER: D-5900
TELECOMUNICATION INFORMATION:
TELEPHONE: 713/651-5246
INFORMATION FOR SEQ ID NO: 436:
LENGTH: 8 base pairs
TYPE: nucleic acid
"ABSOURCE CHARACTERICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
"ABSOURCE CHARACTERICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
"ABSOURCE CHARACTERICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
"ABSOURCE CHARACTERICS:
LENGTH: Base pairs
TYPE: nucleic acid
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) HYPOTHETICAL: YES / ANTI-SENSE: YES US-08-859-954-436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-859-954-437
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MATCHEN, ACTUALLY MORES 12,144

REGISTRANCE/DOCKT NUMBER 13,714

REGISTRANCE/DOCKT NUMBER 13,714

REGISTRANCE/DOCKT NUMBER 13,714

TELECOMORITOR NUMBER 13,714

MATI-GENES 14,717

DESCRIPTIOR NUMBER 14,714

MATI-GENES 14,717

DESCRIPTIOR NUMBER 14,714

MATI-GENES 14,717

DOCUMBER 17,714

APPLICATION DESIGN 10,014

APPLICATION NUMBER 10,014

APPLICATION NUMBER 10,014

COUNTRY 11,014

APPLICATION NUMBER 10,014

APPLICATION NUMBER 10,014

APPLICATION NUMBER 10,014

COUNTRY 11,014

APPLICATION NUMBER 10,014

APPLICATION NUMBER 10,014

COUNTRY 11,014

APPLICATION NUMBER 10,014

APPLICATION NUMBER 10,
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Sequence 37, Application US/08331398A

Patent No. 5608039

GENERAL INFORMATION

APPLICANT: Pastan, Ira

APPLICANT: FitzGerald, David

APPLICANT: FitzGerald, David

APPLICANT: Brinkmann, Ulrich

APPLICANT: Brinkmann, Ulrich

APPLICANT: Brinkmann, Ulrich

APPLICANT: Brinkmann, Ulrich

TITLE OF INVENTION: and Their Uses (as amended)

CORESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Plaza

COUNTRY: USA

ZIP: 94105-149

COMPUTER READABLE FORM:

MEDLING TYPE: Floppy disk
                                                                            DB 1; Length 8;
, 4.6e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 8;
                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
                                                                            25.0%; Score 7; DB 1
100.0%; Pred. No. 4.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.0%; Score 7; DB 1
100.0%; Pred. No. 4.6
tive 0; Mismatches
/desc = "oligonucleotide"
YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
...hes 7; Conservative
                                                                          Query Match
Best Local Similarity 100
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Random Primer
US-09-878-693-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 CCTACGT 12
                                                                                                                                         17 AGGGAGT 23
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                            ; ANTI-SENSE: YES
US-08-859-954-510
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US-08-331-398A-37/c
 DESCRIPTION:
                                                                                                                                                                                                                   RESULT 151
US-09-878-693-5/c
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PELIASSIFICATION DATA:

PELIAGE PRECATOR DATA:

PELIAGE APPLICATION DATA:

NAME: PRICAMIT: 12-CGT-1399

PELIAGE APPLICATION DATA:

PERESTRAIN DATA:

PELIAGE APPLICATION DATA:

PERESTRAIN DATA:
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GENERAL INFORMATION:

APPLICANT: Beathar, Ira
APPLICANT: GO INVENTION: Chimeric and Mutationally Stabilized Tumor
TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Crew
STRET: an Francisco
GUNTR: Son Francisco
GUNTR: USA
COUNTR: USA
COUNTR: USA
COUNTR: USA
COUNTR: IRA PC COMPATION:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 38-60T-994
GLASSIPICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 12-0CT-990
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 156
US-08-759-804A-37/c
i Sequence 37, Application US/08759804A
i Ratent No. 5990296
i GENERAL INFORMATION:
APPLICANT: Pattan: Ira
APPLICANT: Pattan: Ira
APPLICANT: Pattan: Or Interpretation of Interpretation of Interpretation of Interpretation of Invention of Interpretation of Invention of Inven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Sequence 37, Application US/08331397B Patent No. 5981726 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 CAGGGAG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08605163
Patent No. 587988
GENERAL INFORMATION
APPLICANT: Moso, Tommaso
APPLICANT: Tosi, Mario
APPLICANT: Verpy, Blisabeth
APPLICANT: Werby, Blisabeth
APPLICANT: Machol
TITLE OF INVENTION: Method for Detecting Molecules
TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of Base
TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Punner
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                          Query Match 25.0%; Score 7; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET 1300 I Street, N.W.

STATE: D.C.

COUNTY: Washington
STATE: D.C.

COUNTY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/605,163

FILING DATE: 08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MEYEAS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05986.0005-00000
TELECHOWNICAPTON INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
        TYPE: nucleic acid
strandbroness: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-605-163-11
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Best Local Similarity 100.
Matches 7; Conservative
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US-08-331-397B-37/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 154
US-08-605-163-12/c
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; Sequence 37, Application US/09227693
; Patent No. 6287562
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter 6.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 2000:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEPHAX: 650-324-0960
                                                                                                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 158
US-09-227-693-37/c
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TOPOLOGY:
US-09-046-858A-3
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                                      COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IP PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION NUMBER: US/08/759,804A
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/31,398
FILING APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/31,398
FILING APPLICATION DATA:
APPLICATION NUMBER: US/07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/50,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: WEBDE: Ellen L.
RECOMMUNICATION NUMBER: 015280-126140US
TELECOMMUNICATION NUMBER: 015280-126140US
TELECOMMUNICATION NUMBER: 015280-126140US
TELECOMMUNICATION NUMBER: 015280-126140US
TELECOMMUNICATION NUMBER: 015280-126140US
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TELEFAX: 1016ax
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence 3, Application US/09046858A | Sequence 3, Application US/09046858A | Patent No. 6048973 | GENERAL INFORMATION: RADIAGNEZ, RAYMOND L. APPLICANT: ROALTGNEZ, RAYMOND L. TITLE OF INVENTION: IN ALPHA-AMYLASE GENES | TITLE OF INVENTION: IN ALPHA-AMYLASE GENES | CORRESONDENCE ADDRESS: ADDRESSEE Dehlinger & Associates STREET: PO Box 60850 | CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette Diskette Diskette COMPUTER: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION NUMBER: US/09/046,858A FILING DATE: 24-MAR-1998 CLASSIPICATION 800 PRICR APPLICATION BATE: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 60/042,376
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        California
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PRATELL ON CASTAND ITAL APPLICANT: PASTAN ITAL APPLICANT: PASTAN ITAL APPLICANT: BERHAR, ITAL APPLICANT: LEE, PAUNGKOCK TITLE OF INVENTION: FRAGWENTS, FUSION FROTEINS, AND USES THEREOF NUMBER OF SEQUENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCES: TOWNERD AND MARKET PLAZA
STREET: SCHEARL STREET TOWNERD AND MARKET PLAZA
STREET: SCHEARL STREET TOWNERD AND MARKET PLAZA
COUNTRY: CB. TOWNERS: CCOUNTRY: CB. TOWNERS: CCOUNTRY: CB. TOWNERS: US 09/227,693
COUNTRY: CB. TOWNERS: US 09/227,693
COUNTRY: CB. TOWNERS: US 09/227,693
FRILING DATE: DATE:
Query Match
25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indele
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16 CAGGGAG 22
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US-09-989-789-2331
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US-09-989-789-2122
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OTHER INFORMATION: Description of Artificial Sequence: example target
OTHER INFORMATION: DNA
US-02-989-789-2121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Patent No. 6588746

GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: PROSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT APPLICATION NUMBER: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOOTWARRE: Patentin Ver. 2.0

EBNGTH: 9
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                                                                                                                                          25.0%; Score 7; DB 1; Length 9; 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.0%; Score 7; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 0; Indel
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lundeberg, Joaxim
APPLICANT: Lundeberg, Joaxim
APPLICANT: Undeberg, Joaxim
APPLICANT: Undeberg, Joaxim
APPLICANT: Undeberg, Joaxim
APPLICANT: Undeperg, Joaxim
APPLICANT: Undeperg, Joaxim
FILE REFERENCE: 1181-242
CURRENT FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/09153242
Patent No. 6482592
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-227-693-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                           16 CAGGGAG 22
                                                                                                                                                                                                                                                                 CAGGGAG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGCCCT 8
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US-09-989-789-2121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA
US-09-989-789-2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: example target OTHER INFORMATION: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LIU, Olang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 825-0011.20 / $11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2330
                                                                                           Sequence 1221, Application US/09989789
Fatent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, GIANDENT RECOGNITION OF GINN NUCLECTIDE
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GINN NUCLECTIDE
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GINN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRESENCE: 8325-0011.20 / S11-US2
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SEQ ID NO 2122
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.0%; Score 7; DB 1; Les 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.0%; Score 7; DB 1; Le 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 162
US-09-989-789-2330
'Sequence 2330, Application US/09989789
'Patent No. 6588746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100 Matches 7; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: DESCRIPTION of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-2331
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Retent No. 6588746

RAPLICANT: LIU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT FILING DATE: 2502-03-25

NUMBER OF SEQ ID NOS: 4085

SEQ ID NOS: 4085

SEQ ID NO 2348

LENGTH: 9
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Patent No. 6588746
GENERAL INFORMATION
APPLICANT: LIU, Clang
TITLE OF INVENTION: TRIPLERS BY ZINC FINGERS
FILE OF INVENTION: TRIPLERS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / 811-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4086
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2347
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: PRIPETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT PEPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 2331
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.0
Best Local Similarity 100.
Matches 7; Conservative
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US-09-989-789-2348
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| PEATURE: | OTHER INFORMATION: DASCRIPCION OF ARTIFICIAL Sequence: example target | OTHER INFORMATION: DNA US-09-989-789-789-2348
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                                                                                                                    Query Match
25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indeli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE PORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRESESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/450,515
FILING DATE: 29-No. 6680425-1999
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/046,858
FILING DATE: «UNKNOWN)
ATTORNEY/AGENT INFORWATION:
NAWE: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 28,006
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09450515;
Patent No. 6680425;
Patent No. 6680425;
GENERAL INFORMATION:
TITLE OF INVENTION:
IN ALPHA-RAYLASE GENES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
STREET: PO Box 60850;
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 7; DB 1; Le. 100.0%; Pred. No. 4.1e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDARS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 167
US-08-263-790-19/C
; Sequence 19, Application US/09263790
; Patent No. PP12997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
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Best Local Similarity 100.
----hes 7; Conservative
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TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAFF FILE REPERENCE: 2734-102
CURRENT APPLICATION NUMBER: US/09/799, 880
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
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APPLICANT: Khanuja, Suman Preet Singh
APPLICANT: Khanuja, Suman Preet Singh
APPLICANT: Khanuja, Ali Arif
APPLICANT: Kuman, Sushil
ITILE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
FILE REFERENCE: 41799/VGG/X375
CURRENT APPLICATION NUMBER: US/09/785,716A
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Oligonucleotide primer for RAPD profile US-09-785-716A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Patent No. 5861246
GENERAL INFORMATION:
APPLICANT: Sherman Weissman and Girish N. Nallur
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    25.0%; Score 7; DB 1
100.0%; Pred. No. 85;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09799880; Patent No. PP14400; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Banerjee, Suchîtra
Mallavarapu, Gopal
Ramesh, Srinivas
Shasany, Ajit
Darokar, Mahendra
Khanuja, Suman
                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.0
Best Local Similarity 100.
Matches 7; Conservative
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OTHER INFORMATION: Primer US-09-799-880-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GGAGTCC 25
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US-09-799-880-19/c
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LENGTH: 10
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                                                                                                                                                                                                                                                                                                  ; CTHER INFORMATION: MAP 19 Primer - Primer used in RAPD analysis comparing Jal Pallav
; CTHER INFORMATION: with Jorlab-2, Manjusha, Mandakini, Bio-13, and Ceylon.
US-09-263-790-19
GENERAL INFORMATION:

APPLICANT: Nitmal Kumar PATRA et al.

TITLE OF INVENTION:
JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
FILE REPERENCE:
2761-0120P
CURRENT APPLICATION NUMBER: US/09/263,790
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 10
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JAPPLICANT: Runar, Sushil
APPLICANT: Bahl, Janak Faj
APPLICANT: Bahl, Janak Faj
APPLICANT: Bansal, Ravi Prakash
APPLICANT: Nagvi, Shif Ali
APPLICANT: Nagvi, Arif Ali
APPLICANT: Shasan, Jik Kumar
APPLICANT: Singh, Vikram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.0%; Score 7; DB 1; Length 10; 100.0%; Pred. No. 85; 0; Indels vative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 10;
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APPLICANT: Council of Scientific and Industrial Research
APPLICANT: Dwivedi, Samresh
APPLICANT: Singh, Maneesha
APPLICANT: Singh, Maneesha
                                                                                                                                                                                                                                                                                                                                                                                                                25.0%; Score 7; DB 1
100.0%; Pred. No. 85;
iive 0; Mismatches
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CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 12
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 169
US-09-785-716A-18/c
'S Equence 18, Application US/09785716A
'Parent No. PP14090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09538341
Patent No. PP13110
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 GGAGTCC 25
                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GGAGTCC 1
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Gaps
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0
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100.0%; Pred. No. 85;
tive 0; Mismatches
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US-08-388-353-660/c
; Sequence 660, Application US/08388353
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US-08-388-353-659
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                          Conservative
                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GTACAGG 19
                                                                        TOPOLOGY: linear;
MOLECULE TYPE: DNA
US-08-590-571-31
                                                                                                                                                                                                                                                                           18 GGGAGTC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-50-571-31/c
; Sequence 31, Application US/08590571
; Sequence 31, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICAPT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
COUNTRY: USA
                                                                                                      COUNTINE COUNTINE COUNTINE COUNTINE COUNTINE CALLABLE FORM:

MEDIUM TYPE: [Lopy disk COMPUTER: Macintosh OPERATING SYSTEM: MS-DOS SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION NUMBER: US/08/590,571 FILING DATE: CLASSIFICATION NUMBER: US/08/590,571 FILING DATE: CLASSIFICATION: WYMAR: GEOSTEM YANAX REGISTRATION NUMBER: 26,824 REFERENCE/DOCKET NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: £10ppy disk
COMPUTER: Macincosh
OPERATING SYSTEM: Ms-DOS
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,571
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REGISTRATION NUMBER: 26,824
REGISTRATION NUMBER: 26,824
RECISTRATION NUMBER: 26,824
RECOMMUNICATION INPORMATION:
TELEBHONE: (203)268-1951
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (203)268-195
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
                                                                              Connecticut
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STRANDEDNESS: sing
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                                                                                                   USA
                                                   CITY: Tru
STATE: Co
COUNTRY:
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CURRENT APPLICATION DATA:
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| Patent No. 601372
| GENERAL INFORMATION
| GENERAL INFORMATION
| APPLICANT: Barnett, Thomas; Elting, James; Kamarck, Michael;
| APPLICANT: Eartschmer, Axel
| TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
| TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
| TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
| CORRESPONDENCES: 14
| CORRESPONDENCE ADDRESS: ADDRESSE: Sprung HORIN Kramer & Woods
| STRIF: 16940 White Plains Road
| CITY: TATYLYOWN
| STATE: New York CONPUTER: BADABLE FORM: |
| COMPUTER READABLE FORM: | STATEN APPLE MACINTOSH 6500 |
| COMPUTER: APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSERS SCULIA, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City Plaza CITY: Garden City Plaza CIUVIRE: 100 Garden City Plaza CIUVIRE: 100 Garden City STATE: New York CIUVIRE: INEW COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: PLB PC compatible OPERATURG SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NADER: US/08/388,353 PILING DATE: 14-FEB-1995 CLLASSIFICATION: AATORNEY/AGRATION: NAME: Didiglio, Frank S. REGISTRATION NUMBER: 31,346 REFERENCE/DOCKET NUMBER: 31,346 REFERENCE/DOCKET NUMBER: 9606 TELERPHONE: (516) 742-4343: TELERPHONE: (516) 742-4343:
                                                  APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Jennifer C.
APPLICANT: Meximut, Jennifer C.
APPLICANT: Crowe, Suzamne
APPLICANT: Crower, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
WUMBER OF SURVENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.0%; Score 7; I
100.0%; Pred. No.
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US-08-388-353-660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 66
SEQUENCE CHARACTERISTICS:
LENGTH: 10 Dass pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WordPerfect 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 GTACAGG 19
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-468-856B-14
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| PRINCE WINDS WINNERS | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999 | 1999
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GENERAL INFORMATION:
APPLICANT: Barnett, Thomas, Elting, James, Kamarck, Michael, APPLICANT: Kretschmer, Axel
TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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ZIP: 10521-5144

COMPUTER READABLE FORM:
MEDIUM TYRE: Diskette, 3.50 inch, 2.0 Mb storage
COMPUTER: APPLE MACINTOSH 6500
COMPUTER: APPLE MACINTOSH 6500
COMPUTER: APPLE MACINTOSH 6500
CDERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WORDER: US/08/468,859A
FILING DAFE: O6-UN-1995
CLASSIFICATION NUMBER: US 08/027,974
FILING DAFE: US 08/027,974
FILING DAFE: US 08/027,974
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/760,031
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/274,107
FILING DATE: US 07/274,107
FILING DATE: US 07/207,678
FILING DATE: US 07/207,678
FILING DATE: US 07/206,031
FILING DATE: US 08/206,361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sprung Horn Kramer & Woods STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08468859A Patent No. 6022958
                                                                                                                                   (516) 742-4343

TELEFAX: (516) 742-4346

INFORMATION FOR SEQ ID NO: 660: SEQUENCE CHARACTERISTICS: LENGTH: 10 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
                                                 NAME: FRANK S. DIGIGLIO
REPERBORZ/POCKET NUMBER: 96
TELECOMMUNICATION INFORMATION: ($16) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 660 Whit
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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Patent No. 6015661

GENERAL INFORMATION:

APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:

GITY: GARDEN CITY SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER: IBM FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PN364 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 1-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 1-FEB-1995
APPLICATION NUMBER: PN0284
APPLICATION PN0484
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APPLICATION PN0484
APPLICATION PN0484
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APPLICATION PN0484
APPLICATION P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
FILING DATE: 07-UNN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 17-FEB-1995
APPLICATION NUMBER: PN021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: 9606Z
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: 9606Z
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: 9606Z
FILING DATE: 10-MAY-1996
APPLICATION NUMBER: 9606Z
FILING DATE: 10-MAY-1996
APPLICATION NUMBER: 9606Z
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: 9066Z
FI
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Best Local Similarity 100,
Matches 7, Conservative
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                                                                      Sequence 27, Application US/08522384

Patent No. 6110667

GENERAL INFORMATION:
APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: NIGAM, SANJAY KUMAR
TITLE OF INVENTION: PROCESSES, APPRATUS AND COMPOSITIONS FOR TITLE OF INVENTION: PRACESSES, APPRATUS AND COMPOSITIONS FOR TITLE OF INVENTION: 1950-11-15
CURRENT PRILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE PATENTION OF 2.1
SEQ ID NO 27
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-09-313-221A-136/c
| Sequence 136, Application US/09313221A
| Patent No. 6468743 |
| GENERAL INFORMATION: APPLICANT: Thomas L. Romick (Inventor) |
| APPLICANT: Mark S. Praser (Inventor) |
| TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL |
| TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
25.0%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 181
US-09-154-750A-49
; Sequence 49, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION;
; APPLICANT: VOGEIstein, Bert
; APPLICANT: VOGEIstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: FOUPAK, Kornelia
; TITLE REPRENCE: 1107.75557
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.(
Best Local Similarity 100
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 GTCCAGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 AGGGAGT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 GTCCAGG 1
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                                               JS-08-522-384-27/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-154-750A-49
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LENGTH: 10
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Sequence 10, Application US/08906691

Patent No. 6066452

Patent No. 6066452

Patent No. 6066454

Patent No. 7 Series No. 7 Series No. 7 Septicant No. 7 S
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                                                                                                                                                                                                                                                                                                                                                                                                                  25.0%; Score 7; DB 1; Length 10; 100.0%; Pred. No. 85; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/906,691
FILING DATE: 31-UTL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNAY AGENT INFORMATION:
NAME: No. 606452tenburg Ph.D., Carol
NAME: No. 606452tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REBERNCE/DOCKET NUMBER: 390036.403C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID No. 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
TELECOMMUNICATION INPORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INPORMATION FOR ESQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 GGGAGTC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGGCCCT 8
||||||||
1 GGCCCT 7
                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                               US-08-468-859A-14
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APPLICANT: Dawan, Ow Prakash
APPLICANT: Chanula, Suman Preet Singh
APPLICANT: Shaanuja, Suman Preet Singh
APPLICANT: Singh, Seema
APPLICANT: Kumar, Poovappallivadakethil Viswanathan Nair Ajay
APPLICANT: Shabbuddin, Saba
APPLICANT: Shabbuddin, Saba
APPLICANT: Shabbuddin, Saba
APPLICANT: Trivedi, Mala
TITLE OF INVENTION: A novel Streptomyces strain with potential anti-microbial
TITLE OF INVENTION: A novel Streptomyces strain with potential
TITLE OF INVENTION: A novel Streptomyces strain with potential
TITLE OF INVENTION: A novel Streptomyces strain with potential
TITLE OF INVENTION: A novel Streptomyces strain with potential
TITLE OF INVENTION: A novel Streptomyces strain with potential anti-microbial
GURRENT APPLICATION NUMBER: US/09/538,456
GURRENT APPLICATION NOVER: 2000-03-20
MUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Word-97
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                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-151
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                                                                                                                                Length 10;
                                                                                                                                Score 7; DB 1;
Pred. No. 85;
0; Mismatches
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100.0%; Pre
0; !
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100.0%; F.
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Patent No. 6558940
GENERAL INFORMATION:
      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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OTHER INFORMATION: primer
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APPLICANT: Sattar, Abdul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 CCTACGT 12
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Patent No. 6534696

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: A disease resistant high yielding variety Papaver somniferum call

TITLE OF INVENTION: Rakshit

FILE REPRENSE: 086815

CURRENT APPLICATION NUMBER: US/09/537,186

CURRENT FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 13

LENGTH: 10
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                                                                                                                                                                                                                                                                                                                             Gaps
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APPLICANT: Akira SHINAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
APPLICANT: Eiji OHARA
APPLICANT: Eiji OHARA
APPLICANT: Eiji OHARA
CURRENT BERENCE: 00162/46
FILE REFERENCE: 00162/46
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: UP 9/270324
PRIOR APPLICATION NUMBER: UP 9/270324
PRIOR SEQ ID NOS: 472
SEQ ID NO 151
LENGTH: 10
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                                                                                                                                                                                                                                                                                  Length 10;
FILE REFERENCE: HUNT-042784
CURRENT APPLICATION NUMBER: US/09/313,221A
CURRENT FILING DATE: 1999-05-17
PRIOR PRILOK APPLICATION NUMBER: US 60/086,025
PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 136
LENGTH: 10
                                                                                                                                                                                                                                                                                Query Match 25.0%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 85,
Matches 7; Conservative 0; Mismatches
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Sequence 151, Application US/09508753B

Patent No. 6544736

GENERAL INFORMATION:
                                                                                                                                                                                           TYPE: DNA
CRGANISM: Compylobacter jejuni
US-09-313-221A-136
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 7; Conserv
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; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA
US-09-989-789-1285
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25.0%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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// Sequence 1285, Application US/09989789

// Sequence 1285, Application US/09989789

// Patent No. 6588746

// GENERAL INFORMATION:

// APPLICANT: LIV. Qiang

// ITILE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE

// ITILE OF INVENTION: TRIPLETS BY ZINC FINGERS

// ITILE OF INVENTION: TRIPLETS BY ZINC FINGERS

// ITILE OF INVENTION: TRIPLETS BY ZINC FINGERS

// CURRENT APPLICATION NUMBER: US/09/989,789

// CURRENT FILING DATE: 2002-03-25

// NUMBER OF SEQ ID NOS: 4085

// SEQ ID NO 1285

// LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43.

Sequence 43.

Patent No. 656610

GENERAL INFORMATION:

APPLICANT: SRIVASTAVA, SHIV

APPLICANT: WOLL, JUDD W.

TITLE OF INVENTION: POSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: POSTATE-SOUGHOUS

CURRENT APPLICATION NUMBER: 0S/09/769,482

PRIOR PAPLICATION NUMBER: 60/178,772

PRIOR PAPLICATION NUMBER: 60/178,772

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SOFTWARE PATENTING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Description of Artificial Sequence: Synthetic CTHER INFORMATION: oligonucleotide US-09-769-482-43
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0
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100.0%; Pred. No. 85;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches
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                                                                TYPE: DNA

ORGANISM: Artificial sequence

PEATURE:

COTHER INFORMATION: primer

US-09-538-456-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                   19 GGAGTCC 25
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US-09-769-482-43
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LENGTH: 10
                SEQ ID NO 9
LENGTH: 10
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     Gaps
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OTHER INFORMATION: Description of Artificial Sequence: example target
COTHER INFORMATION: DNA
US-09-989-789-1307
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Patent No. 6588746

GENERAL INFORMATION:

APPLICANT: LIU, QIANO

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: PASS-0011.20 / S11-US2

CURRENT APPLICATION DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1314
                                                                                                                                                                                                                                                                      APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT PEPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1307
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0; Indels
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APPLICANT: Mallavarapu, Gopal
APPLICANT: Ramesh, Srinivas
APPLICANT: Ramesh, Srinivas
APPLICANT: Shasmay, Ajit
APPLICANT: Darokar, Mahendra
APPLICANT: Ananuja, Suman
TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAF)
FILE REPERENCE: 2734-102
CURRENT FILE SPECIATION NUMBER: US/09/799,880
CURRENT FILING DATE: 2001-03-07
SOFTWARE: Patentin version 3.1
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Pred. No. 96;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEARTURE; OTHER INFORMATION: Oligonuclectide primer for RAPD profile 38-09-785-716A-18
APPLICANT: Council of Scientific and Industrial Research
APPLICANT: Dwivedi, Samresh
APPLICANT: Singh, Maneesha
APPLICANT: Singh, Maneesha
APPLICANT: Singh, Vandana
APPLICANT: Khanuja, Suman Preet Singh
APPLICANT: Khanuja, Suman Preet Singh
APPLICANT: Kuman, Sushil
                                                                                                                                                                                TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
FILE REFERENCE: 41799/VGG/K375
CURRENT APPLICATION NUMBER: US/09/785,716A
CURRENT FILIG DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 10
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Pred. No. 9
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US-08-388-353-660
; Sequence 660, Application US/08388353
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Patent No. PP14400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kumar, Sushil
APPLICANT: Gupta, Ritika
APPLICANT: Sastry, Kakaraparthi
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80.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Primer US-09-799-880-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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Best Local Similarity
Matches 8; Conserv
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US-09-799-880-19
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ORGANISM: Artificial Sequence
FEATURE:
FORTHER INFORMATION: primer for generating random amplified polymorphic DNA profile of
OTHER INFORMATION: plant
US-09-538-341-12
                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAP 19 Primer - Primer used in RAPD analysis comparing Jal Pallav
; OTHER INFORMATION: with Jorlab-2, Manjusha, Mandakini, Bio-13, and Ceylon.
US-09-263-790-19
                                         Sequence 19, Application US/09263790
Patent No. PP12997
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nitral Kumar PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
CURRENT APPLICATION NUMBER: US/09/263,790
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 10
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Pred. No. 96;
0; Mismatches 2; Indels
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FILE REFERENCE: U-012701-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/538,341
CURRENT FILING DATE: 2000-03-29
NUMBER OS SEQ ID NOS: 13
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shasany, Ajit Kumar
APPLICANT: Darckar, Mahendra Pandurang
APPLICANT: Singh, Vikram
APPLICANT: Sinha, Shweta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Kumar, Sushil
APPLICANT: Bahl, Janak Faj
APPLICANT: Bansal, Ravi Prakash
APPLICANT: Niwas, Shri
APPLICANT: Nagvi, Arif Ali
APPLICANT: Khanuja, Suman, Preet Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 193
US-09-785-716A-18
; Sequence 18, Application US/09785716A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09538341
Patent No. PP13110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.3%;
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Best Local Similarity 80.0°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                               -09-263-790-19
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Gaps
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APPLICANT: Nicholas J. Deacon
APPLICANT: Dai-6 A. McPhee
APPLICANT: David Cooper
ITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-029
MEDLIMITYPE: Floppy disk.
APPLICANT: Learnoit, Januiter C. APPLICANT: Learnoit, Jennifer C. APPLICANT: McPhee, Dale A. APPLICANT: McPhee, Dale A. APPLICANT: Cooper, David APPLICANT: Cooper, David TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1 NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS: ADDRESSE: Scully, Scott, Murphy & Presser STREET: ADDRESSE: Scully, Scott, Murphy & Presser CITY: Garden City Plaza CITY: Garden City STREET: New York COUNTRY: United States
ZIP: 11530
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-PEB-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Patent No. 6015661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTATION UNDRER: 31.346
REPERENCE/DOCKET UNDRER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELERX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 660:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-388-353-660
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-488-551B-660
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IS-09-537-186-13
Sequence 13, Application US/09537186
Sequence 13, Application US/09537186
Sequence 13, Application US/09537186
Batent No. 6534696
GENERAL INFORMATION:
APPLICAMT: COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
TITLE OF INVENTION: A disease resistant high yielding variety Papaver somniferum cal
TITLE OF INVENTION: Rakshit
FILE REPRENEURS: OSB615
CURRENT APPLICATION NUMBER: US/09/537,186
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 14
SCOTWARE: Patentin version 3.1
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: : Primer for generating rank OTHER INFORMATION: m amplified polymorphic DNA profile of claimed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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80.0%; Pred. No. 96;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.3%; Score 6.8;
80.0%; Pred. No. 9
        APPLICATION NOTES.
FILING DATE.
APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: 908/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGHO
NAME: FRANK S. DIGIG
UMBER: US/08/488,551B
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-518-456-9; Sequence 9, Application US/09538456; Patent No. 6558940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear;
; MOLECULE TYPE: DNA
US-08-488-551B-660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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RESULT 200
US-08-487-033-23/c
Sequence 23, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.6%;
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Best Local Similarity 69.2
Matches 9; Conservative
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ORGANISM: HOT
US-08-474-177-23
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                                                  APPLICANT: Xhalique, Abdul
APPLICANT: Zaim, Mohammad
APPLICANT: Zaim, Mohammad
APPLICANT: Trivedi, Mala
TITLE OF INVENTION: A novel Streptomyces strain with potential anti-miorobial
TITLE OF INVENTION: A novel Streptomyces strain with potential anti-miorobial
TITLE OF INVENTION: A novel Streptomyces strain with potential anti-miorobial
TITLE OF INVENTION: A novel Streptomyces strain with potential anti-miorobial
CURRENT EFFENCE: 146920.00003
CURRENT FILING DAIE: 2000-03-20
NUMBER OF SEQ ID NOS: 10
SSOFTWARE: Microsoft Word-97
LENGTH: 10
TYPE: ...
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Patent No. 5624819

GENERAL INFORMATION:

APPLICANT: Skolnick, Mark H.

APPLICANT: Cannon-Albright, Lisa A.

APPLICANT: Kamb, Alexander

ITILE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE

YUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: FILOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/474,177
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATE: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA: DSPLOR APPLICATION DATA: PAPLICATION DATE: PRIOR APPLICATION DATE: DSPLOR APPLICATION DATE: US/08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION DATE: US/08/215,087
FILING DATE: 18-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 6.8; DB
Pred. No. 96;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
COTHER INFORMATION: primer
US-09-538-456-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                    : Alam, Mansoor
: Sattar, Abdul
: Kumar, Sushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 GGAGTCCAGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 deacrecace 10
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 199
US-08-474-177-23/C
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Gaps
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TITLE OP INVENTION: MISIEL-Beta GENE
TITLE OP INVENTION: MISIEL-Beta GENE
TOWBER OF SEQUENCES:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Waahington
STREET: 1201 New York Avenue, Suite 1000
CITY: Waahington
STREET: 20005
COUNTRY: USA
ZIP: 20005
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-UW-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 118-MAR-1995
APPLICATION NUMBER: US 08/215,087
FILING DATE: 118-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6.6; DB 1; Length 16;
Pred. No. 1.9e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              24884-109348-E
PRIOK APPLICATION DATA:

PRIOK APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
RECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810
TENERAL TELEPHONE: 202-962-4810
```

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CATABLE STATES

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington COUNTRY: USA

ZIP: 2005

COMPUTER: ENORY AISK

COMPUTER: ISW PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/508,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6.6; DB 1; Length 16; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGENCIA 223 Application US/08508735

Sequence 23, Application US/08508735

Sequence 23, Application US/08508735

Sequence 23, Application US/08508735

Sequence 23, Application US/08508735

SEQUENCIAL INFORMION:

APPLICANT: Stone, Steven

APPLICANT: Admb, Alexander

TITLE OF INVENTION: MIS GENE AND THERAPEUTIC USE THEREOF

CORRESPONDENCES:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PILING DATE: 07-UN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03316

FILING DATE: 17-WAR-1995

ATTONNEY/AGENT INFORMATION:

NAME: Inhen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4848

TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: YES
ORGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-480-810-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CTACGIGIACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.6
Best Local Similarity 69.2
Matches 9; Conservative
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; Sequence 23, Application US/08480810
; Patent No. 5801236
; GENERAL INFORMATION:
    APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6.6; DB 1; Length 16;
Pred. No. 1.9e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005
ZOUNTRY: USA
ZOUNTRY: USA
COMPUTER READALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/480,810
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
                     PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY, AGBNT INFORMATION:
NAME: Innen, Ueffrey L.
REGISTRATION NUMBER: 24884-109348-C
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION OF 22-862-810
TELEFORMUNICATION OF SEQ ID NO: 23:
SEQUENCE GHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 23.6%;
Best Local Similarity 69.2%;
Matches 9; Conservative
           FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CTACGIGIACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 crrccreakcace 1
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Sequence 23, Application US/08486047
Sequence 23, Application US/08486047
Sequence 23, Application US/08486047
Sequence 25, Application Misself Element No. Sequence 25, Application Alexander TITLE CATT. Kamb. Alexander TITLE CATT. Kamb. Alexander Misself Correspondence Address:
SUMBER OF ENGUNCES: 36
CORRESSE: 1201 New York Avenue, Suite 1000
CITY: Washington CITY: Washington CITY: Washington CITY: Washington CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
COMPUTER: Floopy disk
COMPUTER: Ploopy DATA: APPLICATION DATA: APPLICATION NAMER: US/08/486,047
FILING DATE: 17-MAR-1994
FILING DATE: 17-MAR-1994
FILING DATE: 11-MAR-1994
FILING DATE: 18-MAR-1994
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   REFERENCE/DOCKET NUMBER: 24884-109348-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8310
TELEPHONE: 202-962-8310
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24884-109348-B
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REFERENCE/DOCKET NUMBER: 246
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.6%;
Best Local Similarity 69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 CTACGIGIACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: YES
ORIGINAL SOURCE:
CRGANISM: Homo sapiens
US-08-848-251-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 CTTCCTGGACACG 1
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US-08-848-251-23/c
Sequence 23, Application US/08848251
Patent No. S999815
Patent No. S999815
Patent No. S999815
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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Pred. No. 1.9e+02; 
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAPPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-COMPATED
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/414,083
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/474,083
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 08/251,938
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 10-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 11-APR-1994
ATTORNEY/AGENT INPORMATION:
NUMBER: 11-APR-1994
ATTORNEY/AGENT INPORMATION:
NUMBER: 11-APR-1994
ATTORNEY/AGENT INPORMATION:
NUMBER: 11-APR-1994
ANDER: 11-APR-1994
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
NOLECTLE TYPE: DA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 69.2%;
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CTACGIGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 ctrccreeacace 1
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TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: TYPE: Bingle
TYPE: TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
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                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-120-130-23
                                                                                                                                                                                                                                                                                                                                                                            7 CTACGTGTACAGG 19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Kamb, Alexander
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Mashington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIE: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARENT PAPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24884-109348
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APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,037
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,036
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/27,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/27,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/27,369
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: 11-NON NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ANDOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-120-130-23/c
, Sequence 23, Application US/09120130
; Patent No. 6037462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFRENCE/DOCKET NUMBER: 2488:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPAX: 202-962-8300
                       TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear NOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                ORIGINAL SOURCE:
CRGANISM: Homo sapiens
US-08-486-047-23
                                                                                                                                                                                                                                                                                                                                                                                                                               7 CTACGIGIACAGG 19
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US 09-115-22-27

US 09-115-22

S 09-115-25

S 09-115-25

Patent No. 6060310

Patent No. 6060310

Patent No. 6060310

Patent No. 6060310

TITLE OF INVEXTION: WTSI GENE

CONTESSORINGES:
ADDRESSES: Venable, Beetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STARE: 1201 New York Avenue, Suite 1000

CITY: Washington

STARE: Plopy disk

CONTINE READABLE FORM:

CONTINE READABLE FORM:

CONTINES READABLE FORM:

CONTINES READABLE FORM:

CONTINES TREET: Plopy disk

CONTINES TREET: LOOS/NS.DOS

SOFTWARE: BATENIN RELEASE #1.0, Version #1.30

CONTINES TREET: US 009/480, B10

FILING DATE: 100-1994

PRILING DATE: 17-WAR-1994

PRILING DATE: 18-WAR-1994

PRILING DATE: 18-WA
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Score 6.6; DB 1; Length 16; Pred. No. 1.9e+02; 0; Mismatches 4; Indels
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Gaps

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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICATION
WHER OF SEQUENCES:
ADDRESSE:
VONBESSE:
VONBESSE:
VONBESSE:
VONDICK ADDRESS:
ADDRESSE:
VONDICK ADDRESS:
CONTYRY:
BE SIGNED ON YORK AVENUE, SUITE 1000
CITY:
ABRIGGON
STATE:
COMPUTER:
COMPUTER:
FILD New YORK AVENUE,
MEDIUM TYPE:
FILD NEW YORK AVENUE,
APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
BELLOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
BELLOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
BELLOR APPLICATION DATA:
APPLICATION NUMBER:
BELLOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
F
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; Sequence 23, Application US/09120128
Patent No. 6140473
; GENERAL INFORMATION:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
DOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
NATI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HOMO Sapiens
US-08-986-515-23
                                                                                                                                                                                                                                                                                                                                                                                      23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INFUNCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSE: Venable, Baerjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

STATE: OCCUPANTE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 08/480,810
FILING DATE: US 08/215,936
FILING DATE: US 08/215,936
FILING DATE: US 08/215,036
FILING DATE: US 08/215,036
FILING DATE: US MARR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,369
FILING DATE: US MARR-1994
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: US MARR-1994
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: US MARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: ILENG DATE: US MARR-1994
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-986-515-23/c
; Sequence 23, Application US/08986515
; Patent No. 6090578
                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SERNE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.6%;
ilarity 69.2%;
Conservative (
   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-115-252-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 criccresacace 1
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Best Local Similarity
Matches 9; Conserva
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23.6%; Score 6.6; DB 1; Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09201139
Patent No. 621049
GENERAL INFORMATION:
APPLICANT: Storen
APPLICANT: Storen
APPLICANT: Kamb, Alexander
TILLE OF INVENTION: WTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/201,139
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
PILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey, 1.5.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PARIOR APPLICATION DATA:
PAPPLICATION NUMBER: 08/508,735
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: YES
                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                   Homo sapiens
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SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
LENGIH: 16 base pairs
                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                               ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE
ORGANISM: Hou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC
COUNTRY: USZ
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 210
US-09-201-139-23/c
                                                                                                                                                                                                                                                                                                                                   US-09-120-129-23
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 6.6; DB 1; Length 16; Pred. No. 1.9e+02; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09120129
Patent No. 6180776
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIGNEZ FASEN LINCOLLING TO THE STATE OF THE 
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FLING DATE: 07-UN-1995
PILING DATE: 17-WAR-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-APR-1994
FILING DATE: 14-APR-1994
FILING DATE: 18-WAR-1994
FILING DATE: 18-WAR-1994
FILING DATE: 18-WAR-1994
FILING DATE: 18-WAR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: NUMBER: US 08/214,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 CTTCCTGGACACG 1
LENGTH: 16 base pairs
                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                               ANTI-SENSE: YES

CRIGINAL SOURCE:

CRCANISM: Home

US-09-120-128-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 209
US-09-120-129-23/c
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Indels

Mon Apr 19 15:55:12 2004

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Sequence 34, Application US/0852384

Patent No. 6110667

GENERAL INFORMATION:
APPLICANT: LOPEZ-INFTO, CARLOS E
APPLICANT: LOPEZ-INFTO, CARLOS E
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6.4; DB 1; Length 10;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE;
; OTHER INFORMATION: Description of Unknown Organism:
US-08-522-844-34
    Best Local Similarity 69.2%; Pred. No. 1.9e+02; Matches 9; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.9%;
Best Local Similarity 87.5%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.9%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown Organism
                                                                       7 CTACGTGTACAGG 19
                                                                                                             13 chrechegacace 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 CGTGTACA 17
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                                                                                                                                                                                                  US-08-522-384-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 34
LENGTH: 10
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                            Gaps
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  Pred. No. 1.9e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                    Sequence 23, Application US/09120131
Patent No. 6318146
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION:
WIMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24884-109348-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: BCT/US95/03316
FILING DATE: 17-WAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA: US 08/215,087
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/215,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
ATTORNEY/ABORT INFORMATION:
NAME: INDEN, Jeffrey L.
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                  7 CTACGTGTACAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202-962-8300
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nucleic acid
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ORIGINAL SOURCE:
ORGANISM: HOMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
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STATE: DC
COUNTRY:
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US-09-425-798-12

Sequence 12. Application US/09425798A

Patent No. 6423433

Patent No. 6423433

GENERAL INFORMATION:
APPLICANT: Gorenteein Dr., David G.
APPLICANT: King Dr., David J.
APPLICANT: Wentura, Daniel A.
APPLICANT: Brasier Dr., Allan R.
APPLICANT: Brasier Dr., Allan R.
APPLICANT: On On On One of Phosphothionate
ITILE OF INVENTION: Oligonuclectide Aptamers
FILE REPERENCE: 122144-1005

CURRENT APPLICATION NUMBER: US/09/425,798A

CURRENT FILING DATE: 1999-10-25

PRIOR FILING DATE: 1999-10-26

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 12

LENGTH: 10

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 6.4; DB 1; Length 10;
Pred, No. 1.2e+02;
0; Mismatches 1; Indels
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DB 1; Length 16;

23.6%; Score 6.6;

Query Match

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Sequence 30, Application US/09153242;
Sequence 30, Application US/09153242;
Patent No. 6482592;
GENERAL INFORMATION:
APPLICANT: Unlen, Mathias
TITLE OF INVENTION: MODULAR PROBES II
FILE REFERENCE: 1181-242;
CURRENT PALICATION NUMBER: US/09/153,242;
CURRENT FILING DATE: 1999-09-15;
PRIOR FILING DATE: 1997-09-26;
NUMBER OF SEQ ID NOS: 63;
SOOFWARE: Patentin Ver: 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
CURRENT FILING DATE: 2002-C
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2453
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
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Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                    Sequence 24, Application US/08319492B
Sequence 24, Application US/08319492B
Setent No. 56488
GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TILLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESPONDED. ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 5.5" Diskette, 1.60

SOFTWARE: FORMER: 100 Mp. C. DOS 5.0

SOFTWARE: More Perfect 5.1

CURRENT APPLICATION DATA: 10944

PRIOR APPLICATION DATA: including application prior APPLICATION DATA: including application PRIOR APPLICATION DATA: 10994

PRIOR APPLICATION NUMBER: 08/008, 895

FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989, 849

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg Richard

REFERENCE/DOCKET NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 30,9276

TELECOMMUTICATION INFORMATION:

METERRENCE/DOCKET NUMBER: 30,9276
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 Date pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.1
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-989-789-2453
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; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA
US-09-989-789-2453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: example target , OTHER INFORMATION: DNA US-09-989-789-2454
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2454. Application US/09989789

Patent No. 6588746

GENERAL INFORMATION:
APPLICANT: LIU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERRANCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SSOTIMARE: PREFENTIN VET. 2.0
SSO ID NO 2454
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                 DB 1; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                              Query Match
21.4%; Score 6; DB 1; Len
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0;
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Mon Apr 19 15:55:12 2004
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US-09-153-242-33/c
US-09-153-242-33/c

Sequence 33, Application US/09153242

Retent No. 6482592
GENERAL INFORMATION:
APPLICANT: Undeberg, Joakim
PRIOR PERENEUR: 1994-09-15
PRIOR APPLICATION NUMBER: US/09/153,242
CURRENT APPLICATION NUMBER: PCT/GB97/02629
PRIOR PALING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 33
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
COTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: Oligonucleotide H3
US-09-153-242-33
                                                                                                                                     0; Gaps
                                                                               Query Match
21.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
; OTHER INFORMATION: oligonucleotide H1-9 US-09-153-242-30
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0; Gaps

Query Match 21.4%; Score 6; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 4.18+02; Matches 6; Conservative 0; Mismatches 0; Indels

2 GGGCCC 7 |||||| 7 GGGCCC 2 Search completed: April 19, 2004, 15:06:49 Job time: 1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:

April 19, 2004, 15:10:53 ; Search time 0.001 Seconds (without alignments) 68.488 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-024-396-3-COPY 28 1 cgggccctacgtgtacagggagtccagg 28

IDENTITY\_NUC Gapop 10.0 , Gapext 0.5 Scoring table:

95 seqs, 1223 residues Searched:

190 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 132 summaries

Database :

Published - Applications NA \*:qpqd

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Appl	Appl	App,	Appl	Appl																						Appl	Appl	Appl	Appl			
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
SUMMARIES		! #	4-	-08-983-605-2	-09-853-105-1	-09-918-	-10-159-856-3	-10-159-856-1	-10-184-372-2	-09-882-945	-09-930-423	-09-930-423-104	-09-930-4	-09-745-237A-64	-09-745-237A-10	-09-745-237A-112	-09-818-875-295	-09-818-875-295	ò	-10-156-306-702	-10-238-700-308	-10-209-787-295	-10-209-787-295	-10-261-185-295	-10-261-185-295	-09-504-231A-14	-09-274-553D-14	-10-407-637-2	-09-879-813-7	09-912-6	10-146-505-7	8-10-193-507-8	S-09-504-231A-	-274-553D-31
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Sequence 51, Appl Sequence 61, Appl Sequence 137, Appl Sequence 137, Appl Sequence 137, Appl Sequence 137, Appl Sequence 29, Appl Sequence 29, Appl Sequence 24, Appl Sequence 24, Appl Sequence 14, Appl Sequence 125, Appl Sequence 27, Appl Sequence 21, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 2195, Appl Sequence 2453, Appl Sequence 2454, Appl Sequen	equence 37, equence 37, equence 52, equence 52, equence 16, equence 16, equence 16, equence 17, equence 17, equence 17, equence 17, equence 17, equence 27, equenc
US-10-193-507-51 US-08-591-486B-61 US-09-274-2311-137 US-09-274-5311-137 US-09-274-5311-137 US-09-274-65 US-09-989-364-67 US-09-989-364-67 US-09-989-364-67 US-10-330-627-29 US-10-330-627-125 US-10-330-627-125 US-10-330-627-125 US-10-330-627-125 US-10-330-627-125 US-10-330-627-125 US-10-330-627-125 US-10-330-627-125 US-10-344-206-86 US-10-344-206-86 US-10-344-206-86 US-10-344-206-86 US-10-344-306-19 US-10-34-396-209 US-10-34-396-209 US-09-990-186-2195 US-09-990-186-2195 US-09-990-186-2195 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-186-2453 US-09-990-980-994-2454	S. 10-376-341-97 S. 10-0276-341-97 S. 10-027-522-32 S. 10-027-522-32 S. 10-027-52-52 S. 10-037-52-52 S. 10-033-145-16 S. 10-033-145-16 S. 10-033-627-46 S. 10-033-627-46 S. 10-033-627-46 S. 10-239-185-17 S. 10-223-1155-17 S. 10-223-125-23 S. 10-027-632-17 S. 10-223-126-17 S. 10-104-307-24 S. 10-103-938-2 S. 10-103-938-2 S. 10-103-938-8 S. 10-203-787-29 S. 10-203-787-29
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-203
                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.7
Best Local Similarity 84.2
Matches 16; Conservative
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US-09-853-105-19
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Publication No. US20030147864A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
FILLE REPERENCE: RIS-0339
CURRENT APPLICATION NUMBER: US/10/024,396
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 91
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                    US-10-024-396-19/c
US-10-024-396-19/c
Sequence 19, Application US/10024396
Publication No. US20030147864A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
FILE OF INVENTION: ANYISENSE MODULATION OF CD36L1 EXPRESSION
FILE REPERENCE: RTS-0339
CURRENT APPLICATION NUMBER: US/10/024,396
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 91
: LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.4%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 20; Conservative 0; Mismatches 0; Indels
                                                OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                               ALIGNMENTS
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US-10-024-396-20/c
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APPLICANT: Roder, Marion
TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
TITLE OF INVENTION: Triticum Asstivum and Tribe Triticase and the Use of
TITLE OF INVENTION: Said Markers
CURRENT APPLICATION NUMBER: US/08/983,605A
CURRENT FILING DATE: 1998-05-01
EARLIER APPLICATION NUMBER: DE 195 25 284.5
EARLIER TILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 466
SEQ ID NO 203
SEQ ID NO 203
LENGTH: 19
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| Publication No. US20030149236A1 |
| Publication No. US20030149236A1 |
| GENERAL INFORMATION: DOUGLAS J. |
| TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR NUMBER OF SEQUENCES: 25 |
| CORRESPONDENCE ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States of America ZIP: 11530 |
| COMPUTER READABLE FORM: | MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION: | MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC COMPATION: | MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC COMPATION: | MEDIUM TYPE: Platen IDM PC COMPATION: | MEDIUM TYPE: PLATEN | MEDIUM TYPE: | MED
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Pred. No. 5;
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 20; Conservative 0; Mismatches
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84.2%; Pred. No. 5;
'... 0; Mismatches
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-396-20
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FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/853,105
FILING DATE: 10-May-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-983-605-203/c
Sequence 203, Application US/08983605A; Publication No. US20020066118A1
; GENERAL INFORMATION:
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4 GCCCTACGTGTACAGGGA 21
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                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                         PRIOR FILING DATE: 2000-08-16
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-159-856-105
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US-10-159-856-105
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APPLICANT: Stone, David
APPLICANT: Stone, David
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT APPLICATION NUMBER: G0/221,409
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR PELING DATE: 2000-08-08
PRIOR PELING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: G0/223,752
PRIOR APPLICATION NUMBER: G0/223,762
PRIOR PELING DATE: 2000-08-08
PRIOR PELING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: G0/225,146
PRIOR PELING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.7%; Score 14.2; DB 1; Length 21;
84.2%; Pred. No. 6.1;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-853-105-19
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 10296
TELEROMENDICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFEX: (516) 742-4366
TELEFX: (516) 742-4366
TELEFX: 203 901 SANS UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
APPLICANT: Paddigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Spaderna, Steven
APPLICANT: Shinkers, Richard
APPLICANT: Zerhusen, Bryan
APPLICANT: Zerhusen, Bryan
APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Kimberly
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10. US20030064369A1
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Gusev, Vladimir
Grase, William
Alsobrook, John
Lepley, Denise
Burgess, Catherine
Gerlach, Valerie
Ellerman, Karen
MacDougall, John
Stone, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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Sequence 105, Application US/10159856
Publication No. US20030228689A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
ANTICANT: Semeth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPITIER REFERENCE: RTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 105
LENGTH: 20
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US-10-159-856-39/C

US-10-159-856-39/C

Sequence 39, Application US/10159856

Publication No. U320030228689A1

GENERAL INFORMATION:
APPLICANT: Susan M. Freier

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPIRITE REFERENCE: RTS-0365

CURRENT APPLICATION NUMBER: US/10/159,856

CURRENT PILLING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 134

LENGTH: 20

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide; OTHER INFORMATION: primers
US-09-918-779-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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47.9%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 8.5;
Matches 14; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 15; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Antisense Oligonucleotide US-10-159-856-39
PRIOR APPLICATION NUMBER: 60/263,662
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/281,645
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 35
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US-09-930-423-1045/c
| Sequence 1045, Application US/0930423
| Sequence 1045, Application US/0930423
| Publication No. US20030092003A1
| GENERAL INFORMATION:
| APPLICANT: Blatt, Larry
| APPLICANT: Blatt, Larry
| APPLICANT: McSwiggen, Jim
| TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
| FILE REFERENCE: MBH00, 918-A 400/027
| CURRENT APPLICATION NUMBER: US0/09/930, 423
| CURRENT FILING DATE: 2001-08-15
| SOFTWARE: Patentin version 3.0
| SEQ ID NOS: 4553
| SOFTWARE: Patentin version 3.0
                                                                                                        Publication No. US2003092003A1

Sequence 643, Application US/09930423

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blatt, Larry
APPLICANT: BHBOO, 918-A 400/027

CURRENT APPLICATION WINHER: US/99/930, 423

CURRENT FILING DATE: 2001-08-15

WINHER OF SEQ ID NOS: 4553

SEQ ID NO 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McGwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MEBBOO, 918-A, 400/027
CURRENT APPLICATION NUMBER: US/09/930,423
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Pred. No. 18
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Pred. No. 18
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  1 GGACCCTATGTCTACAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1045
                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
Matches 12; Conserv
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                                                                            RESULT 10
US-09-930-423-643/c
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APPLICANT: Lyamichev, Victor
APPLICANT: Allawi, Hatim
APPLICANT: Dong, Fang
APPLICANT: Neri, Bruce
APPLICANT: Neri, Bruce
APPLICANT: Neri, Tainan
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
FILE REPERENCE: FORS-04586
CURRENT APPLICATION NUMBER: US/09/882,945A
CURRENT FILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 334
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
LENGTH: 17
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47.1%; Score 13.2; DB 1; Length 20;
llarity 83.3%; Pred. No. 9.4;
Conservative 0; Mismatches 3; Indels
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Pred. No. 13;
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Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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US-09-882-945A-275
                                                                          4 GCCCTACGTGTACAGGGA
                                                                                                              2 GCGCATCGTGTACAGGGA
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Best Local Similarity 92.9
Matches 13; Conservative
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COTHER INFORMATION: primer US-10-184-372-23
              Best Local Similarity
Matches 15; Conserv
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    Query Match
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2 GGGCCCTACGTGTACAG 18

17 GTGTACAGCGAGT

2001-08-15

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Sequence 2950, Application US/09818875

Sequence 2250, Application US/09818875

Publication No. US20030051270A1

GENERAL INFORMATION:

APPLICANT: Kined, Etc. B.

APPLICANT: Rice, Michael C.

TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single

TITLE OF INVENTION: Stranded Oligonucleotides

TILE REFERENCE: Napro-4

CURRENT APPLICATION NUMBER: US/09/818,975

CURRENT FILING DATE: 2001-03-27

PRIOR PILING DATE: 2000-03-27

PRIOR PILING DATE: 2000-03-27

PRIOR PILING DATE: 2000-06-01

PRIOR PILING DATE: 2000-06-01

PRIOR PILING DATE: 2000-06-01

PRIOR PILING DATE: 2000-06-01

PRIOR SPLING DATE: 2000-06-01

PRIOR PILING DATE: 2000-06-01

PRIOR SPLING DATE: 2000-06-01

NUMBER OF SEG ID NOS: 4385

SOFTWARE: Friedman macro Napro4

LEMICH 177
                                                                                                                                                       Sequence 1120, Application US/09745237A
Publication No. US20030143708A1
Publication No. US20030143708A1
GENERAL INFORMATION:
PAPPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLIC
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81.2%; Pred. No. 20;
sive 0; Mismatches 3;
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92.3%;
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Best Local Similarity 81.2
Matches 13; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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US-09-818-875-2950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1120
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US-09-818-875-2951
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Publication No. US20030143708A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: WcSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
TIER PERRENCE: 400/007 (MBHBN0-918-A)
CURRENT APPLICATION NUMBER: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1045
LENGTH: 17
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Publication No. US20030143708A1
Publication No. US20030143708A1
Publication No. US20030143708A1
APPLICANT: NIPORMATION:
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Method and Reagent for the Treatment of Alzheimer's Disease FILE REPERENCE: 400/007 (MBHB00-918-A)
CURRENT PELING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: Patentin version 3.0
SEQ ID NO 643
LENGTH: 17
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40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels
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Pred. No. 18;
0; Mismatches
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CURRENT FILING DATE: 2001-08-1
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: Patentin version 3.0
SEQ ID NO 1120
LENGTH: 17
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.3%;
Matches 12; Conservative
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ORGANISM: Homo sapiens
                                                                                                                           : LENGTH: 17
: TYPE: RNA
: ORGANISM: Homo Sapiens
US-09-930-423-1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Homo sapiens
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US-09-745-237A-1045/c
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US-09-745-237A-643/c
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Sequence 3087, Application US/10238700
; Sequence 3087, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: McSwiggen, James
    TITE OF INVENTION: NUCLEIC Acid Treatment of Diseases or Conditions Related to Lev.
    FILE REFERENCE: 400/057 (WHHB01-1158-A)
    CURRENT APPLICATION NUMBER: US/10/238,700
    CURRENT APPLICATION NUMBER: PCT/US 02/16840
    FRIOR FILING DATE: 2002-05-29
    FRIOR FILING DATE: 2002-05-29
    FRIOR FILING DATE: 2001-09-10
    NUMBER OF SEQ ID NOS: 4666
    SOFTWARE PatentIn version 3.0
    SEQ ID NO 3087
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| Sequence 2556, Application US/10209787
| Publication No. US20030217377A1
| CENERAL INPORMATION:
| APPLICANT: Kniec, Exica B. APPLICANT: Rice, Michael C. TILLS OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single ITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single ITLE OF INVENTION: Stranded Oligonucleotides FILE OF INVENTION: Stranded Oligonucleotides FILE REFERENCE: Napro-4
| TURENT APPLICATION NUMBER: US 109/818,875 |
| PRIOR APPLICATION NUMBER: US 60/192,176 |
| PRIOR PILING DATE: 2000-03-27 |
| PRIOR PILING DATE: 2000-03-27 |
| PRIOR PILING DATE: 2000-03-27 |
| PRIOR PILING DATE: 2000-03-27 |
| PRIOR PILING DATE: 2000-03-27 |
| PRIOR PILING DATE: 2000-03-27 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-06-01 |
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| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-06-01 |
| PRIOR PILING DATE: 2000-08-07 |
| PRIOR PILING DATE: 2000-08-07 |
| PRIOR PILING DATE: 2000-08-07 |
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| PRIOR PILING DATE: 2000-08-07 |
| PRIOR PILING DATE: 2000-08-08 |
| PRIOR PILING DATE: 2000-08-08 |
| PRIOR PILING DATE: 2000-08 |
| PRIOR PILING DATE: 2000-08 |
| PRIOR PILING DATE: 2000-08
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Best Local Similarity 75.0%; Pred. No. 20;
Matches 12; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11.2; Pred. No. 20;
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF EGO ID NOS: 8013
SOFTWARE: Patentin version 3.0
SEQ ID NO 7027
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68.8%;
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Best Local Similarity 68.8
Matches 11; Conservative
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CORGANISM: Homo sapiens
US-10-238-700-3087
                                                                                                                                                                                                                                                                                                      TYPE: RNA
CORGANISM: Homo sapiens
US-10-156-306-7027
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Publication No. US20030119017A1
GENERAL INFORMATION No. WESONOTHER PROPERTY.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Levels of IKK-Gamma and PKR
                                                                                         JOHNSTON TRAINER, Exic B.

APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
TITLE OF INVENTION: Stranded Oligonucleotides
TITLE OF INVENTION: Stranded Oligonucleotides
TITLE OF INVENTION: Stranded Oligonucleotides
TITLE OF INVENTION WINNER: US 60/192,176
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
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Sequence 7026, Application US/10156306
Publication No. US20030119017A1
GENERAL INFORMATION:
BAPPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION UNMER: US/10/156,306
CURRENT APPLICATION OFFER: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: Pacentin version 3.0
SOFTWARE: Pacentin version 3.0
LENGTH: 17
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68.8%; Pred. No. 20;
tive 2; Mismatches
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Best Local Similarity 81.2%;
Matches 13; Conservative (
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                          US20030051270A1
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; ORGANISM: Homo sapiens
US-10-156-306-7026
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US-09-818-875-2951
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Matches 11; Conserv
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US-10-156-306-7027
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APPLICANT: Gamper, Howard B.

APPLICANT: Gamper, Howard B.

APPLICANT: Gamper, Howard B.

APPLICANT: Rice, Michael C.

ITILE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
ITILE OF INVENTION: Stranded Oligonucleotides

TILE OF INVENTION: Stranded Oligonucleotides

FILE REFERNCE: NaPro-4CON

CURRENT APPLICATION NUMBER: US/10/261,185

CURRENT FILING DATE: 2002-09-27

PRIOR APPLICATION NUMBER: US 60/192,176

PRIOR APPLICATION NUMBER: US 60/192,179

PRIOR PILING DATE: 2000-03-27

PRIOR APPLICATION NUMBER: US 60/224,989

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 4385

SEQ ID NOS: 4385
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40.0%; Score 11.2; D

Best Local Similarity 81.2%; Pred. No. 20;

Matches 13; Conservative 0; Mismatches
  PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/204,939
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SOFTWARE: Friedman macro Napro4
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; Sequence 2951, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 143, Application US/09504231A
Patent No. US20020013458A1
GENERAL INFORMATION:
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; APPLICANT: McSwiggen, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ACGIGIACAGGGAGIC
                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-2950
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US-10-261-185-2951
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Best Local Similarity
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US-09-504-231A-143
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USS-10-209-787-2951

Sequence 2951, Application US/10209787

Sequence 2951, Application US/10209787

Sequence 2951, Application O. US20030217377A1

Sequence 2951, Application O. US20030217377A1

GENERAL INFORMATION:
APPLICANT: General Movard B.
APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard C.
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REPRENCE: Narc-4

CURRENT APPLICATION NUMBER: US/10/209, 787

CURRENT FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: US 60/192,176

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 4385

SEQ ID NOS: 4385

LENGTH: 17
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Publication No. US20040014057A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kmiec, Eric B.
APPLICANT: Kmiec, Michael C.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Tarageted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: NaPro-4CON
CURRENT APPLICATION NUMBER: US/10/261,185
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: PCT/US01/09761
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Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                 Query Match

40.0%; Score 11.2; I
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SOFTWARE: Friedman macro Napro4
SEQ ID NO 2950
LENGTH: 17
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CORGANISM: Homo sapiens
US-10-209-787-2951
                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-2950
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NAME/KEY: misc_feature
LOCATION: (7).-(10)
OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC
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CURRENT APPLICATION NUMBER: US 60/372,352
PRIOR APPLICATION NUMBER: US 60/372,675
PRIOR FILING DATE: 2002-04-12
PRIOR PILING DATE: 2002-04-15
PRIOR FILING DATE: 2002-04-15
PRIOR PILING DATE: 2002-04-15
PRIOR PRIOR FILING DATE: 2002-04-15
PRIOR PRIOR PLICATION NUMBER: US 60/421,010
PRIOR PRIOR PLICATION NUMBER: US 60/421,010
PRIOR PLING DATE: 2002-04-15
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PRIOR PLING DATE: 2002-04-15
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Facento No. US20020155453A1
GENERAL INFORMATION:
APPLICANT: Sale, Julian E.
APPLICANT: Neuberger, Michael S.
TITLE OF INVENTION: Method of Generating Diversity
FILE REFERENCE: 18396/2005
CURRENT APPLICATION NUMBER: US/09/879,813
CURRENT FILING DATE: 2001-06-11
FRIOR RILING DATE: 2001-06-11
FRIOR RILING DATE: 1999-10-06
FRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.1
SEQ ID NO 73
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SEQ ID NO 73
SEQ ID NO 73
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Pred. No. 15;
0; Mismatches 1;
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80.0%; Pred. No. 26;
                                                                                                                                                                 ; Sequence 20, Application US/10407637; Publication No. US20030194736A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: mutated pUC19
US-10-407-637-20
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: unknown
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US-09-879-813-73/c
                                                                            RESULT 27
US-10-407-637-20/c
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                       APPLICANT: Pavo, Pamela

APPLICANT: Pavo, Pamela

APPLICANT: Pavo, Pamela

APPLICANT: Macelak, Dennis

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

CURRENT APPLICATION NUMBER: 09/504,231A

CURRENT FILING DATE: 1999-02-15

FRIOR FILING DATE: 1999-02-24

FRIOR PLING DATE: 1999-02-24

FRIOR PLING DATE: 1999-02-24

FRIOR PLING DATE: 1999-04-18

FRIOR PLING DATE: 1998-09-18

FRIOR FILING DATE: 1998-04-18

FRIOR FILING DATE: 1998-04-18

FRIOR FILING DATE: 1998-04-18

FRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3242

SEQ ID NOS: 3242

SEQ ID NO 143

LENGTH: 15
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ORGANISM: Artificial Sequence
FEATURE:
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Roberts, Beth
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LOCATION: (7)..(110)
OTHER INFORMATION: F264
OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC
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Publication No US20030108889A1
GENERAL INFORMATION:
APPLICANT: Sale, Julian E.
APPLICANT: Cumbers, Sarah J.
TITLE OF INVENTION: Method of Generating Diversity
FILE REFERENCE: 18396/2005B
CURRENT PELLOTION UNDER: US/10/146,505
CURRENT PELLOTION UNDER: 09/828,717
PRIOR APPLICATION NUMBER: 09/879,813
PRIOR APPLICATION NUMBER: 09/879,813
PRIOR APPLICATION NUMBER: 09/879,813
PRIOR PILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: GB 9822104.7
PRIOR APPLICATION NUMBER: GB 982104.7
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-01-19
PRIOR PILING DATE: 1999-01-19
                                                                                                                       APPLICANT: Ye, Bangee
TITLE OF INVENTION: MEDIUM AND LOW DENSITY GENE CHIPS
FILE REFERENCE: UNB 100
CURRENT PPLICATION NUMBER: US/09/912,673A
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO S.55
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10.2; D
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: P(qs)1 DNA probe US-09-912-673A-55
                            Sequence 55, Application US/09912673A Publication No. US20030186230A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0%;
Matches 12; Conservative
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-673A-55/c
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FATERIT NO. UNZUUZUO13458A1

GARDERAL INFORMATION:
APPLICANT: BLACK, LAWTENCE
APPLICANT: ROBERTS, Dames
APPLICANT: ROBERTS, Beth
APPLICANT: ROBERTS, Beth
APPLICANT: ROBERTS, Beth
APPLICANT: ROBERTS, Beth
APPLICANT: PavCo, Pamela
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APPLICANT: PavCo, Pamela
APPLICANT: PavCo, Pamela
APPLICANT: PavCo, Pamela
APPLICANT: PavCo, Pamela
APPLICANT: PavCo, Pamela
APPLICANT: PavCo, Pamela
APPLICANTON: HERATHEN C VIRUS INFECTION
TITLE OF INVENTION: HERATHIS C VIRUS INFECTION
TITLE OF INVENTION NUMBER: 09/09/504,231A
CURRENT FILING DATE: 1999-02-15
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICANTON NUMBER: 60/083,217
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 3242
SERIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 3242
SERIOR FILING DATE: Patentin version 3.0
SECTAMES PATENTIN VERSION 3.0
SECTAMES PATENTIN VERSION 3.0
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US-09-504-231A-319
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Best Local Similarity 90.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                         APPLICANT: Anastasio, Alison E.
APPLICANT: Anastasio, Amir
APPLICANT: Academica, Mainael F.
APPLICANT: Lachowica, Michael F.
APPLICANT: Bachow, Vicente
APPLICANT: Shah, Nisha
TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE
FILE REFERENCE: MWH-2790US
CURRENT APPLICATION NUMBER: US/10/193,507
CURRENT FILING DATE: 2002-07-12
PRIOR FILLING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentin version 3.1
: SEQ ID NO 83
LENGTH: 10
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100.0%; Pred. No. 13;
tive 0; Mismatches (
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                  Sequence 83, Application US/10193507
Publication No. US20040018493A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
COGANISM: Homo sapiens
US-10-193-507-83
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US-09-504-231A-319
-10-193-507-83
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APPLICANT: Schlingensiepen, Georg F
APPLICANT: Schlingensiepen, Rarl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Gotingen, Wolfgang Brysch
TITLE OF INVENTION: A Pharmacoutical Composition
TITLE OF INVENTION: Of Neuronal Injury, Degeneration and Cell Death and for the
TITLE OF INVENTION: Treatment of Neoplasms
NUMBER OF SEQUENCES: 185
CORRESPONDENCES ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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CONRESPONDENCE ADDRESS:
STREET: 400 Seventh Street, N.W.
CITY: Washington, D.C
COUWIRY: 0.S.A.
ZIP: 2004
COMPUTER READABLE FORM:
MEDIUTYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,486B
FILING DATE: 11-JAN-1995
CLASSIFICATION NUMBER: EP 93111059.7
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 10-JUL-1993
PRIOR APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 10-JUL-1993
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 1,0996/P60122
TELEBOOMMUNICATION INFORMATION:
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Pred. No. 28;
0; Mismatches 2; Indels
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                                                                                                                                                                                  ; Sequence 61, Application US/08591486B
; Publication No. US20020037866Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
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84.6%;
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TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 61.
SEQUENCE CHARACTERISTICS:
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15 ACAGGGAGTC 24
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Best Local Similarity
Matches 11; Conserva
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MOLECULE TYPE:
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US-09-504-231A-137
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US-08-591-486B-61
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APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Mcejak, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISBASES OR CONDITIONS RELATE
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REPRENCE: rpi 247/282
CURRENT APPLICATION NUMBER: US/09/274,553D
CURRENT PILING DATE: 1999-03-23
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APPLICANT: Anactasio, Amir
APPLICANT: Lacionaica, Michael F.
APPLICANT: Lacionaica, Michael F.
APPLICANT: Pabon, Vicente
APPLICANT: Shah, Nieha
TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE
FILE REFERENCE: MMH-2790US
CURRENT APPLICATION NUMBER: US/10/193,507
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: 60/304,573
PRIOR APPLICATION NUMBER: 60/304,573
PRIOR FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentin version 3.1
LENGTH: 15
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PRIOR APPLICATION NUMBER: 09/257,608

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1998-09-18

PRIOR PLILING DATE: 1998-09-18

PRIOR PLILING DATE: 1998-04-7

NUMBER OF SEQ ID NOS: 3148

SOFTWARE: PATENTIN VETSION 3.0

SEQ ID NO 319

LENGTH: 15
                                                                                                                                                                                     Sequence 319, Application US/09274553D
Patent No. US20020082225A1
GENERAL INFORMATION:
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Publication No. US20040018493A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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19 GGAGTCCAGG 28
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US-10-193-507-51
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Pred. No. 26;
0; Mismatches 1; Indels
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APPLICANT: Nathberg, Jonathan M
APPLICANT: Nathberg, Girish N
APPLICANT: Hu, Xinghua
TITLE OF INVENTION: Methods and Devices for Measuring
TITLE OF INVENTION: Differential Gene Expression
FILE REFERENCE: 7934-05.
CURRENT APPLICATION NUMBER: US/09/989,364
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/203,231
PRIOR APPLICATION NUMBER: 09/203,231
PRIOR PLING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: oligonucleotide US-10-113-877-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.6%;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.6%;
2 GCCCCUACGUAUA 14
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Best Local Similarity 90.9
Matches 10; Conservative
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; OTHER INFORMATION: Primer
US-09-989-364-67
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US-09-989-364-67
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                  APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REFERENCE: rpi 247/282
CURRENT APPLICATION NUMBER: US/09/504,231A
CURRENT APPLICATION NUMBER: 09/274,553
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3242
SOFTWARE: PALENTH Version 3.0
SEQ ID NO 137
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICANT: Blatt, Lawrence
APPLICANT: Blatt, Lawrence
APPLICANT: Blatt, Lawrence
APPLICANT: McSwigen, James
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Macelak, Dennis
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILLE REFERENCE: 129 24.723
FILLE REFERENCE: 129 2.03-23
FILLE REFERENCE: 129 2.02-24
FRIOR APPLICATION NUMBER: 60/100,842
FRIOR APPLICATION NUMBER: 60/003,217
FRIOR APPLICATION NUMBER: 60/003,217
FRIOR FILLING DATE: 1998-04-27
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US-09-274-553D-137
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35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred, No. 32;
Matches 8; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 137, Application US/09274553D Patent No. US20020082225A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GGCCCTACGTGTA 15
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APPLICANT: Blatt, Lawrence
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US-09-274-553D-137
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ccraccrerac 12

3 GGCCCTACGTGTA 15

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Sequence 26, Application US/10104307
Sequence 26, Application US/10104307
Sequence 26, Application WS/203018072941
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: POWDRILL, Tom
APPLICANT: HOGAN, Michael
TITLE OF INVENTION: Hybridization Rate Enhancement for Substrate-Bound Specific Nuc
TITLE OF INVENTION: Binding Agents
FILE REFERENCE: 053960,0001/1US
FILE REFERENCE: 053960,0001/1US
CURRENT APPLICATION NUMBER: US/10/104,307
CURRENT PILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 36
SOUTHARE: Patentin version 3.0
SEQ ID NO 26
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10;
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Sequence 67, Application US/09989364

Publicacion No. US20030003463A1

SERENEAL INFORMATION:
APPLICANT: Nallur, Girish N

APPLICANT: Hu, Xinghua and Devices for Measuring TITLE OF INVENTION: Differential Gene Expression

TITLE OF INVENTION: Differential Gene Expression

TITLE OF INVENTION WINGER: US/09/989,364

CURRENT APPLICATION NUMBER: 09/203,231

PRIOR APPLICATION NUMBER: 09/203,231

PRIOR APPLICATION NUMBER: 09/203,231

PRIOR APPLICATION NUMBER: 09/203,231

SEQUENCE: SEQUENCE: THE SECUENCE: THE SECUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ore 9; DB 1;
red. No. 23;
Mismatches
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Pred. No. 35;
0; Mismatches
FILE REPERENCE: 001107.00119
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SEQ ID NO 29
LENGTH: 10
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ORGANIGM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Primer
US-09-989-364-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-330-627-29
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Best Local Similarity
Matches 9; Conserva
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US-10-104-307-26
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APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Rail-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
TITLE OF INVENTION: A Pharmaceutical Composition
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment of Number OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Hohman & Stern
STREET: 400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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COUNTRY 2004

COMPUTER READABLE FORM;
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM; PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,486B
FILING DATE: 11-JAN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: EP 93111059.7
FILING DATE: 10-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 0-JUL-1993
RPIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 0-JUL-1993
RPIOR APPLICATION NUMBER: 13,409
REPERENCE/DOCKET NUMBER: 10496/P60122
TEDECOMMUTCATION INFORMATION:
MAME: PLAYON NUMBER: 10496/P60122
TEDECOMMUTCATION INFORMATION:
MEDICATION NUMBER: 10496/P60122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh Street, N.W. CITY: Washington, D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.9%; Score 9.2; DE Best Local Similarity 78.6%; Pred. No. 38; Matches 11; Conservative 0; Mismatches
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APPLICANT: Kinzler, Kenneth W
APPLICANT: Kinzler, Bert
TILE OF INVENTION: Human Transcriptomes
                                                                                                                                                Application US/08591486B
. US20020037866A1
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US-10-330-627-29
; Sequence 29, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 638-6666
TELEFAX: (202) 333-395.0
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 164:
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E: DNA (genomic)
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LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLICATION MOLECULE TYPE: D.
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US-08-591-486B-164
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APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
APPLICANT: MOUL, JUDD W.
APPLICANT: WINDAM TAKEHIKO
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
FILE REFERENCE: 04995. 0057-00000
CURRENT APPLICATION NUMBER: US/10/390,045
CURRENT FILING DATE: 2003-03-18
PRIOR PILING DATE: 2003-03-18
PRIOR PILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/179,72
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
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                                                                                                                                                                    Score 8.4; DB 1; Length 10;
Pred. No. 31;
0; Mismatches 1; Indels
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Pred. No. 31;
0; Mismatches 1; Indels
                                                                                             ; OTHER INFORMATION: Synthetic oligonucleotide US-10-329-465-242
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CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR APPLICATION NUMBER: US 09/448,480
NUMBER OF SEQ ID NOS: 1564
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Publication No. US20030175771A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/10390045; Publication No. US20030170713A1; GENERAL INFORMATION:
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                       30.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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US-10-330-627-1257/c
                                                                         FEATURE:
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Publication No. US20030165949A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLITILE OF INVENTION: FUSION
TITLE OF INVENTION: FUSION
TITLE REPERBACE: 27373/329,465
CURRENT APPLICATION NUMBER: US/10/329,465
PRIOR APPLICATION NUMBER: US 60/343,826
PRIOR FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 315
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Publication No. US20030176374A1

GENERAL INFORMATION:
APPLICANT: Wickers, Timothy A.
APPLICANT: Wickers, Timothy A.
APPLICANT: Wickers, Timothy A.
APPLICANT: Wickers, Timothy A.
APPLICANT: Wickers, Timothy A.
APPLICANT: Wickers, Timothy A.
APPLICANT: Wickers, Timothy A.
APPLICANT: Night and Methods for the TILE OF INVENTION: Oligomolectide Compositions and Methods for the TILE OF INVENTION: Modulation of the Expression of B7 Protein FILE REPRENCE: 1584-033

CURRENT APPLICATION NUMBER: DC7/US00/14471

PRICA PLICATION NUMBER: 09/326,186

PRICA PLICATION NUMBER: 09/326,186

PRICA PLICATION NUMBER: 09/326,186

PRICA FILING DATE: 1999-06-04

PRICA RELIGATION NUMBER: 08/777,266

PRICA FILING DATE: 1999-16-12-31

NUMBER OF SEQ ID NOS: 284

SEQ ID NO 85

LENGTH: 10
                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                          ; DB 1; Length 13;
                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                        Score 8.8; DB
Pred. No. 40;
0; Mismatches
                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic US-09-851-871-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 44
US-09-851-871-85/c
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